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Grimaldi, J. Christopher
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Kljavin, Ivar J.
Kuo, Sophia S.
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Phe Ala Phe Ala Glu Leu Cys Val Val Pro Leu Arg Ile Phe Ser
                365                 370                 375

Phe Phe Pro Val Pro Val Thr Val Arg Ala His Leu Thr Gly Trp
                380                 385                 390

Leu Met Thr Leu Lys Lys Thr Phe Val Leu Ala Pro Ser Ser Val
                395                 400                 405

Leu Arg Ile Ile Val Leu Ile Ala Ser Leu Val Val Leu Pro Tyr
                410                 415                 420

Leu Gly Val His Gly Ala Thr Leu Gly Val Gly Ser Leu Leu Ala
                425                 430                 435

Gly Phe Val Gly Glu Ser Thr Met Val Ala Ile Ala Ala Cys Tyr
                440                 445                 450

Val Tyr Arg Lys Gln Lys Lys Lys Met Glu Asn Glu Ser Ala Thr
                455                 460                 465

Glu Gly Glu Asp Ser Ala Met Thr Asp Met Pro Pro Thr Glu Glu
                470                 475                 480

Val Thr Asp Ile Val Glu Met Arg Glu Glu Asn Glu
                485                 490
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<210> 8
<211> 535
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 66, 96, 387
<223> unknown base

<400> 8
 cctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50

 tgagcttctg gtgccntttg gctctaattc tggccacaca gagaancagt 100

 cggcctattg tcaacctctt tgtttcccgg gaccttggtg gcagttctgc 150

 agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200

 tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250

 aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300

 ggcccacatc aagaagttca ccttcgtctg catggctctg tcactcacgc 350

 tctgtttcgt gatgttttgg acacccaacg tgtctgngaa aatcttgata 400

 gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450
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gcggatcttc tccttcttcc cagttccagt cacagtgagg gcgcatctca 500

ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,
293, 296, 305, 336, 358, 361
<223> unknown base

<400> 9
tgacggaatc ccgggctggg tatcctggtt tngacaagat aaaccccccag 50

caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100

agttcacctt ngtttgnatg gntctgtcaa ctcacgctnt gtttcgtgat 150

gttttggaca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200

tggantttgc ctttgcagaa ntttgngntg ttcctttgcg gattttctcc 250

tttttcccag ttccagtcac agngagggcg catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350

ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400

gcgaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10
<211> 154
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 49, 68, 83, 90, 98, 119
<223> unknown base

<400> 10
tattcccagt tccggtcacg gggagggcgc atntcaccgg gtggctgang 50

acactgaaga aaaccttngt ccttgccccc agntttgtgn tgcggatnat 100

cgtcctcatc gccagcctng tggtcctacc ctacctgggg gtgcacggtg 150

agac 154

<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctgatccggt tcttggtgcc cctg 24

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
gctctgtcac tcacgctc 18

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
tcatctcttc cctctccc 18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccttccgcca cggagttc 18

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
ggcaaagtcc actccgatga tgtc 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
gcctgctgtg gtcacaggtc tccg 24

<210> 17
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18
<211> 1901
<212> DNA
<213> Homo sapiens

<400> 18
gccccgcgcc cggcgccggg cgcccgaagc cgggagccac cgccatgggg 50

gcctgcctgg gagcctgctc cctgctcagc tgcgcgtcct gcctctgcgg 100

ctctgccccc tgcatcctgt gcagctgctg ccccgccagc cgcaactcca 150

ccgtgagccg cctcatcttc acgttcttcc tcttcctggg ggtgctggtg 200

tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250

ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300

tcgactgtgg ctccctgctt ggctaccgcg ctgtctaccg catgtgcttc 350

gccacggcgg ccttcttctt cttctttttc accctgctca tgctctgcgt 400

gagcagcagc cgggaccccc gggctgccat ccagaatggg ttttggttct 450

ttaagttcct gatcctggtg ggcctcaccg tgggtgcctt ctacatccct 500

gacggctcct tcaccaacat ctggttctac ttcggcgtcg tgggctcctt 550

cctcttcatc ctcatccagc tggtgctgct catcgacttt gcgcactcct 600

ggaaccagcg gtggctgggc aaggccgagg agtgcgattc ccgtgcctgg 650

tacgcaggcc tcttcttctt cactctcctc ttctacttgc tgtcgatcgc 700

ggccgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg 750

agggcaaggt cttcatcagc ctcaacctca ccttctgtgt ctgcgtgtcc 800

atcgctgctg tcctgcccaa ggtccaggac gcccagccca actcgggtct 850

gctgcaggcc tcggtcatca ccctctacac catgtttgtc acctggtcag 900

ccctatccag tatccctgaa cagaaatgca acccccattt gccaacccag 950

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ctgggcaacg agacagttgt ggcaggcccc gagggctatg agacccagtg 1000

gtgggatgcc ccgagcattg tgggcctcat catcttcctc ctgtgcaccc 1050

tcttcatcag tctgcgctcc tcagaccacc ggcaggtgaa cagcctgatg 1100

cagaccgagg agtgcccacc tatgctagac gccacacagc agcagcagca 1150

gcaggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg 1200

tcacctacag ctactccttc ttccacttct gcctggtgct ggcctcactg 1250

cacgtcatga tgacgctcac caactggtac aagcccggtg agacccggaa 1300

gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350

cagggctgct cctctacctg tggaccctgg tagccccact cctcctgcgc 1400

aaccgcgact tcagctgagg cagcctcaca gcctgccatc tggtgcctcc 1450

tgccacctgg tgcctctcgg ctcggtgaca gccaacctgc cccctcccca 1500

caccaatcag ccaggctgag cccccacccc tgccccagct ccaggacctg 1550

cccctgagcc gggccttcta gtcgtagtgc cttcagggtc cgaggagcat 1600

caggctcctg cagagcccca tccccccgcc acacccacac ggtggagctg 1650

cctcttcctt cccctcctcc ctgttgccca tactcagcat ctcggatgaa 1700

agggctccct tgtcctcagg ctccacggga gcggggctgc tggagagagc 1750

ggggaactcc caccacagtg ggcatccgg cactgaagcc ctggtgttcc 1800

tggtcacgtc ccccagggga ccctgccccc ttcctggact tcgtgcctta 1850

ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900

a 1901

<210> 19
<211> 457
<212> PRT
<213> Homo sapiens

<400> 19
Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser
 1               5                  10                  15

Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro
                20                  25                  30

Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe
                35                  40                  45

Leu Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly
                50                  55                  60
```

Val Glu Ser Gln Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly
65 70 75

Ala Gly Ile Pro Thr Val Leu Gln Gly His Ile Asp Cys Gly Ser
80 85 90

Leu Leu Gly Tyr Arg Ala Val Tyr Arg Met Cys Phe Ala Thr Ala
95 100 105

Ala Phe Phe Phe Phe Phe Phe Thr Leu Leu Met Leu Cys Val Ser
110 115 120

Ser Ser Arg Asp Pro Arg Ala Ala Ile Gln Asn Gly Phe Trp Phe
125 130 135

Phe Lys Phe Leu Ile Leu Val Gly Leu Thr Val Gly Ala Phe Tyr
140 145 150

Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe Tyr Phe Gly Val
155 160 165

Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val Leu Leu Ile
170 175 180

Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys Ala Glu
185 190 195

Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe Thr
200 205 210

Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe
215 220 225

Met Tyr Tyr Thr Glu Pro Ser Gly Cys His Glu Gly Lys Val Phe
230 235 240

Ile Ser Leu Asn Leu Thr Phe Cys Val Cys Val Ser Ile Ala Ala
245 250 255

Val Leu Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu
260 265 270

Gln Ala Ser Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser
275 280 285

Ala Leu Ser Ser Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro
290 295 300

Thr Gln Leu Gly Asn Glu Thr Val Val Ala Gly Pro Glu Gly Tyr
305 310 315

Glu Thr Gln Trp Trp Asp Ala Pro Ser Ile Val Gly Leu Ile Ile
320 325 330

Phe Leu Leu Cys Thr Leu Phe Ile Ser Leu Arg Ser Ser Asp His
335 340 345

Arg Gln Val Asn Ser Leu Met Gln Thr Glu Glu Cys Pro Pro Met

```
                    350                 355                 360

Leu Asp Ala Thr Gln Gln Gln Gln Gln Gln Val Ala Ala Cys Glu
                365                 370                 375

Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly Val Thr Tyr Ser Tyr
                380                 385                 390

Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser Leu His Val Met
                395                 400                 405

Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr Arg Lys Met
                410                 415                 420

Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala Ser Trp
                425                 430                 435

Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu Leu
                440                 445                 450

Leu Arg Asn Arg Asp Phe Ser
                455

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
 gccgcctcat cttcacgttc ttcc 24

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 21
 tcatccagct ggtgctgctc 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 22
 cttcttccac ttctgcctgg 20

<210> 23
<211> 18
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 23
cctgggcaaa aatgcaac 18

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
caggaatgta gaaggcaccc acgg 24

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
tggcacagat cttcacccac acgg 24

<210> 26
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27
<211> 1351
<212> DNA
<213> Homo sapiens

<400> 27
gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50

ttaacctggg tcaaatgcac ggattctcac ctcgtacagt tacgctctcc 100

cgcggcacgt ccgcgaggac ttgaagtcct gagcgctcaa gtttgtccgt 150

aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200

tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250 actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300

cccagagccc tattacccgg aatctggatg ggaccgcctc cgggagctgt 350

ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400

aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450

agcttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500

tttatcataa ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca 550

cgaggcttca ttcgttatgg ctggcgctgg ggttggagaa ctgcagtgtt 600

tgtgactata ttcaacacag tgaacactag tctgaatgta taccgaaata 650

aagatgcctt aagccatttt gtaattgcag gagctgtcac gggaagtctt 700

tttaggataa acgtaggcct gcgtggcctg gtggctggtg gcataattgg 750

agccttgctg ggcactcctg taggaggcct gctgatggca tttcagaagt 800

acgctggtga gactgttcag gaaagaaaac agaaggatcg aaaggcactc 850

catgagctaa aactggaaga gtggaaaggc agactacaag ttactgagca 900

cctccctgag aaaattgaaa gtagtttacg ggaagatgaa cctgagaatg 950

atgctaagaa aattgaagca ctgctaaacc ttcctagaaa cccttcagta 1000

atagataaac aagacaagga ctgaaagtgc tctgaacttg aaactcactg 1050

gagagctgaa gggagctgcc atgtccgatg aatgccaaca gacaggccac 1100

tctttggtca gcctgctgac aaatttaagt gctggtacct gtggtggcag 1150

tggcttgctc ttgtcttttt cttttctttt taactaagaa tggggctgtt 1200

gtactctcac tttacttatc cttaaattta aatacatact tatgtttgta 1250

ttaatctatc aatatatgca tacatggata tatccaccca cctagatttt 1300

aagcagtaaa taaaacattt cgcaaaagat taaagttgaa ttttacagtt 1350

t 1351

<210> 28
<211> 285
<212> PRT
<213> Homo sapiens

<400> 28

Met	Glu	Val	Pro	Pro	Pro	Ala	Pro	Arg	Ser	Phe	Leu	Cys	Arg	Ala
1				5					10					15
Leu	Cys	Leu	Phe	Pro	Arg	Val	Phe	Ala	Ala	Glu	Ala	Val	Thr	Ala
				20					25					30

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Asp Ser Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val
                35                  40                  45

Pro Glu Pro Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu
                50                  55                  60

Leu Phe Gly Lys Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala
                65                  70                  75

Asn Ile Cys Lys Thr Ala Ala Thr Ala Gly Ile Ile Gly Trp Val
                80                  85                  90

Tyr Gly Gly Ile Pro Ala Phe Ile His Ala Lys Gln Gln Tyr Ile
                95                  100                 105

Glu Gln Ser Gln Ala Glu Ile Tyr His Asn Arg Phe Asp Ala Val
                110                 115                 120

Gln Ser Ala His Arg Ala Ala Thr Arg Gly Phe Ile Arg Tyr Gly
                125                 130                 135

Trp Arg Trp Gly Trp Arg Thr Ala Val Phe Val Thr Ile Phe Asn
                140                 145                 150

Thr Val Asn Thr Ser Leu Asn Val Tyr Arg Asn Lys Asp Ala Leu
                155                 160                 165

Ser His Phe Val Ile Ala Gly Ala Val Thr Gly Ser Leu Phe Arg
                170                 175                 180

Ile Asn Val Gly Leu Arg Gly Leu Val Ala Gly Gly Ile Ile Gly
                185                 190                 195

Ala Leu Leu Gly Thr Pro Val Gly Gly Leu Leu Met Ala Phe Gln
                200                 205                 210

Lys Tyr Ala Gly Glu Thr Val Gln Glu Arg Lys Gln Lys Asp Arg
                215                 220                 225

Lys Ala Leu His Glu Leu Lys Leu Glu Glu Trp Lys Gly Arg Leu
                230                 235                 240

Gln Val Thr Glu His Leu Pro Glu Lys Ile Glu Ser Ser Leu Arg
                245                 250                 255

Glu Asp Glu Pro Glu Asn Asp Ala Lys Lys Ile Glu Ala Leu Leu
                260                 265                 270

Asn Leu Pro Arg Asn Pro Ser Val Ile Asp Lys Gln Asp Lys Asp
                275                 280                 285
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<210> 29
<211> 324
<212> DNA
<213> Homo sapiens

<400> 29
cggaagtccc ttgaggagcg tcagaagcgg cttccctacg tcccagagcc 50

ctattacccg gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100

tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150

ctacagcagg catcattggc tgggtgtatg gggaatacc agcttttatt 200

catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250

ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300

ttcgttcatg gctggcgccg aacc 324

<210> 30
<211> 377
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 262, 330, 371
<223> unknown base

<400> 30
tcaagtttgt ccgtaggtcg agagaaggcc atggaggtgc cgccaccggc 50

accgcggagc ttttttctgt agagcattgt gcctatttcc ccgagttttt 100

gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150

gcggcttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200

gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250

cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300

gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350

agagccaggc agaaatttat nataacc 377

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 31
tcgtacagtt acgctctccc 20

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 32
cttgaggagc gtcagaagcg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
ataacgaatg aagcctcgtg 20

<210> 34
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 34
gctaatatct gtaagacggc agctacagca ggcatcattg 40

<210> 35
<211> 1819
<212> DNA
<213> Homo sapiens

<400> 35
gagccgccgc cgcgcgcgcg ccgcgcactg cagccccagg ccccggcccc 50

ccacccacgt ctgcgttgct gccccgcctg ggccaggccc caaaggcaag 100

gacaaagcag ctgtcaggga acctccgccg gagtcgaatt tacgtgcagc 150

tgccggcaac cacaggttcc aagatggttt gcgggggctt cgcgtgttcc 200

aagaactgcc tgtgcgccct caacctgctt tacaccttgg ttagtctgct 250

gctaattgga attgctgcgt ggggcattgg cttcgggctg atttccagtc 300

tccgagtggt cggcgtggtc attgcagtgg gcatcttctt gttcctgatt 350

gctttagtgg gtctgattgg agctgtaaaa catcatcagg tgttgctatt 400

tttttatatg attattctgt tacttgtatt tattgttcag ttttctgtat 450

cttgcgcttg tttagccctg aaccaggagc aacagggtca gcttctggag 500

gttggttgga acaatacggc aagtgctcga aatgacatcc agagaaatct 550

aaactgctgt gggttccgaa gtgttaaccc aaatgacacc tgtctggcta 600

gctgtgttaa aagtgaccac tcgtgctcgc catgtgctcc aatcatagga 650

gaatatgctg gagaggtttt gagatttgtt ggtggcattg gcctgttctt 700 cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750

agaaagaccc ccgcgcgaat cctagtgcat tcctttgatg agaaaacaag 800

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ggtggcacct ggaatttact gtattcattg tcgggcactg tccactgtgg 1050

cctttcttag catttttacc tgcagaaaaa ctttgtatgg taccactgtg 1100

ttggttatat ggtgaatctg aacgtacatc tcactggtat aattatatgt 1150

agcactgtgc tgtgtagata gttcctactg gaaaaagagt ggaaatttat 1200

taaaatcaga aagtatgaga tcctgttatg ttaagggaaa tccaaattcc 1250

caattttttt tggtcttttt aggaaagatt gttgtggtaa aaagtgttag 1300

tataaaaatg ataatttact tgtagtcttt tatgattaca ccaatgtatt 1350

ctagaaatag ttatgtctta ggaaattgtg gtttaatttt tgacttttac 1400

aggtaagtgc aaaggagaag tggtttcatg aaatgttcta atgtataata 1450

acatttacct tcagcctcca tcagaatgga acgagttttg agtaatcagg 1500

aagtatatct atatgatctt gatattgttt tataataatt tgaagtctaa 1550

aagactgcat tttaaacaa gttagtatta atgcgttggc ccacgtagca 1600

aaaagatatt tgattatctt aaaaattgtt aaataccgtt ttcatgaaat 1650

ttctcagtat tgtaacagca acttgtcaaa cctaagcata tttgaatatg 1700

atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatattct 1750

gttaaaaaat taaaggacag aaacctttct ttgtgtatgc atgtttgaat 1800

taaaagaaag taatggaag 1819

<210> 36
<211> 204
<212> PRT
<213> Homo sapiens

<400> 36

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Met Val Cys Gly Gly Phe Ala Cys Ser Lys Asn Cys Leu Cys Ala
  1               5                  10                  15

Leu Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile
                 20                  25                  30
```

```
Ala Ala Trp Gly Ile Gly Phe Gly Leu Ile Ser Ser Leu Arg Val
                35                  40                  45

Val Gly Val Val Ile Ala Val Gly Ile Phe Leu Phe Leu Ile Ala
                50                  55                  60

Leu Val Gly Leu Ile Gly Ala Val Lys His His Gln Val Leu Leu
                65                  70                  75

Phe Phe Tyr Met Ile Ile Leu Leu Leu Val Phe Ile Val Gln Phe
                80                  85                  90

Ser Val Ser Cys Ala Cys Leu Ala Leu Asn Gln Glu Gln Gln Gly
                95                  100                 105

Gln Leu Leu Glu Val Gly Trp Asn Asn Thr Ala Ser Ala Arg Asn
                110                 115                 120

Asp Ile Gln Arg Asn Leu Asn Cys Cys Gly Phe Arg Ser Val Asn
                125                 130                 135

Pro Asn Asp Thr Cys Leu Ala Ser Cys Val Lys Ser Asp His Ser
                140                 145                 150

Cys Ser Pro Cys Ala Pro Ile Ile Gly Glu Tyr Ala Gly Glu Val
                155                 160                 165

Leu Arg Phe Val Gly Gly Ile Gly Leu Phe Phe Ser Phe Thr Glu
                170                 175                 180

Ile Leu Gly Val Trp Leu Thr Tyr Arg Tyr Arg Asn Gln Lys Asp
                185                 190                 195

Pro Arg Ala Asn Pro Ser Ala Phe Leu
                200
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<210> 37
<211> 390
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336
<223> unknown base

<400> 37
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tgattggagc tgtaaaaaan tcttcaggtg ttgtnatttt tttatatgat 50

tattctgtaa nttgtattta ttgttcagtt ttntgtatct tgcgcttgtt 100

tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150

aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200

gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250

gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300
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gaggttttga gatttgttgg tggcattggc ctgttnttca gttttacaga 350

gatcctgggt gtttggctga cctacagata caggaaccag 390

<210> 38
<211> 566
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 27
<223> unknown base

<400> 38
aatcccaaat tccccaattt ttttggnctt tttagggaaa gatgtgttgt 50

ggtaaaaagt gttagtataa aaatgataat ttacttgtag tcttttatga 100

ttacaccaat gtattctaga atagttatgt cttaggaaat tgtggtttaa 150

tttttgactt ttacaggtaa gtgcaaagga gaagtggttt catgaaatgt 200

tctaatgtat aataacattt accttcagcc tcccatcaga atggaacgag 250

ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300

taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350

ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400

ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450

gcatatttga atatgatctc ccataatttg aaattgaaat cgtattgtgt 500

ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550

gttgtgcccc acttgc 566

<210> 39
<211> 264
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 84-85, 206
<223> unknown base

<400> 39
atgattattc tgttacttgt atttattgtt cagttttatg gtatcttgcg 50

cttgtttagc ccctgaaacc aggagcaaca gggnncagct tcctggaggt 100

tggttggcaa caatcacggc caagtgactc cgcaaatgac atcccagaga 150

aatcctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200 tggctngctg tgttaaaagt gaccactcgt gctcgccatg tgctccaatc 250

ataggagaat atgc 264

<210> 40
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 40
acccacgtct gcgttgctgc c 21

<210> 41
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 41
gagaatatgc tggagagg 18

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 42
aggaatgcac taggattcgc gcgg 24

<210> 43
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
ggccccaaag gcaaggacaa agcagctgtc agggaacctc cgccg 45

<210> 44
<211> 2061
<212> DNA
<213> Homo sapiens

<400> 44
cagtcaccat gaagctgggc tgtgtcctca tggcctgggc cctctacctt 50

tcccttggtg tgctctgggt ggcccagatg ctactggctg ccagttttga 100

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gacgctgcag tgtgagggac ctgtctgcac tgaggagagc agctgccaca 150
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tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat 250
cctccaaggt ccagccaagc cagtttttga aggggacctg ctggttctgc 300
gctgccaggc ctggcaagac tggccactga ctcaggtgac cttctaccga 350
gatggctcag ctctgggtcc ccccgggcct aacagggaat tctccatcac 400
cgtggtacaa aaggcagaca gcgggcacta ccactgcagt ggcatcttcc 450
agagccctgg tcctgggatc ccagaaacag catctgttgt ggctatcaca 500
gtccaagaac tgtttccagc gccaattctc agagctgtac cctcagctga 550
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tgcagaggtc agctgcccgc ctcctcttct ccttctacaa ggatggaagg 650
atagtgcaaa gcaggggggct ctcctcagaa ttccagatcc ccacagcttc 700
agaagatcac tccgggtcat actggtgtga ggcagccact gaggacaacc 750
aagtttggaa acagagcccc cagctagaga tcagagtgca gggtgcttcc 800
agctctgctg cacctcccac attgaatcca gctcctcaga aatcagctgc 850
tccaggaact gctcctgagg aggcccctgg gcctctgcct ccgccgccaa 900
ccccatcttc tgaggatcca ggcttttctt ctcctctggg gatgccagat 950
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accagaagcc tgggaccaca aaggctactg ctgaatagaa gtaaacagtt 1100
catccatgat ctcacttaac caccccaata aatctgattc tttattttct 1150
cttcctgtcc tgcacatatg cataagtact tttacaagtt gtcccagtgt 1200
tttgttagaa taatgtagtt aggtgagtgt aaataaattt atataaagtg 1250
agaattagag tttagctata attgtgtatt ctctcttaac acaacagaat 1300
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tgatttaaag agaactaatg gaagtggatt gaatacagca gtctcaactg 1400
ggggcaattt tgcccccccag aggacattgg gcaatgtttg gagacatttt 1450
ggtcattata cttggggggt tgggggatgg tgggatgtgt gtctactggc 1500
atccagtaaa tagaagccag gggtgccgct aaacatccta taatgcacag 1550
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ggcagtaccc cacaacgaaa aataatctgg cccaaaatgt cagttgtact 1600

gagtttgaga aaccccagcc taatgaaacc ctaggtgttg ggctctggaa 1650

tgggactttg tcccttctaa ttattatctc tttccagcct cattcagcta 1700

ttcttactga cataccagtc tttagctggt gctatggtct gttctttagt 1750

tctagtttgt atcccctcaa aagccattat gttgaaatcc taatccccaa 1800

ggtgatggca ttaagaagtg ggcctttggg aagtgattag atcaggagtg 1850

cagagccctc atgattagga ttagtgccct tatttaaaaa ggccccagag 1900

agctaactca cccttccacc atatgaggac gtggcaagaa gatgacatgt 1950

atgagaacca aaaaacagct gtcgccaaac accgactctg tcgttgcctt 2000

gatcttgaac ttccagcctc cagaactatg agaaataaaa ttctggttgt 2050

ttgtagccta a 2061

<210> 45
<211> 359
<212> PRT
<213> Homo sapiens

<400> 45

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Met Lys Leu Gly Cys Val Leu Met Ala Trp Ala Leu Tyr Leu Ser
 1               5                  10                  15

Leu Gly Val Leu Trp Val Ala Gln Met Leu Leu Ala Ala Ser Phe
                20                  25                  30

Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser
                35                  40                  45

Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe
                50                  55                  60

Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val
                65                  70                  75

Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe
                80                  85                  90

Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp
                95                 100                 105

Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly
               110                 115                 120

Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys
               125                 130                 135

Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro
               140                 145                 150
```

```
Gly Pro Gly Ile Pro Glu Thr Ala Ser Val Val Ala Ile Thr Val
                155                 160                 165

Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala Val Pro Ser Ala
                170                 175                 180

Glu Pro Gln Ala Gly Ser Pro Met Thr Leu Ser Cys Gln Thr Lys
                185                 190                 195

Leu Pro Leu Gln Arg Ser Ala Ala Arg Leu Leu Phe Ser Phe Tyr
                200                 205                 210

Lys Asp Gly Arg Ile Val Gln Ser Arg Gly Leu Ser Ser Glu Phe
                215                 220                 225

Gln Ile Pro Thr Ala Ser Glu Asp His Ser Gly Ser Tyr Trp Cys
                230                 235                 240

Glu Ala Ala Thr Glu Asp Asn Gln Val Trp Lys Gln Ser Pro Gln
                245                 250                 255

Leu Glu Ile Arg Val Gln Gly Ala Ser Ser Ser Ala Ala Pro Pro
                260                 265                 270

Thr Leu Asn Pro Ala Pro Gln Lys Ser Ala Ala Pro Gly Thr Ala
                275                 280                 285

Pro Glu Glu Ala Pro Gly Pro Leu Pro Pro Pro Pro Thr Pro Ser
                290                 295                 300

Ser Glu Asp Pro Gly Phe Ser Ser Pro Leu Gly Met Pro Asp Pro
                305                 310                 315

His Leu Tyr His Gln Met Gly Leu Leu Leu Lys His Met Gln Asp
                320                 325                 330

Val Arg Val Leu Leu Gly His Leu Leu Met Glu Leu Arg Glu Leu
                335                 340                 345

Ser Gly His Gln Lys Pro Gly Thr Thr Lys Ala Thr Ala Glu
                350                 355
```

<210> 46
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 46
tgggctgtgt cctcatgg 18

<210> 47
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 47
tttccagcgc caattctc 18

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
agttcttgga ctgtgatagc cac 23

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
aaacttggtt gtcctcagtg gctg 24

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51
<211> 2181
<212> DNA
<213> Homo sapiens

<400> 51
cccacgcgtc cgcccacgcg tccgcccacg ggtccgccca cgcgtccggg 50

ccaccagaag tttgagcctc tttggtagca ggaggctgga agaaaggaca 100

gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150

gcacctaaca gtggacactt atggccgtcc catcctggaa gtgccagaga 200

gtgtaacagg accttggaaa ggggatgtga atcttccctg cacctatgac 250

cccctgcaag gctacaccca agtcttggtg aagtggctgg tacaacgtgg 300

ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc 350 agcaggcaaa gtaccagggc cgcctgcatg tgagccacaa ggttccagga 400

gatgtatccc tccaattgag caccctggag atggatgacc ggagccacta 450

cacgtgtgaa gtcacctggc agactcctga tggcaaccaa gtcgtgagag 500

ataagattac tgagctccgt gtccagaaac tctctgtctc caagcccaca 550

gtgacaactg gcagcggtta tggcttcacg gtgccccagg gaatgaggat 600

tagccttcaa tgccaggctc ggggttctcc tcccatcagt tatatttggt 650

ataagcaaca gactaataac caggaaccca tcaaagtagc aaccctaagt 700

accttactct tcaagcctgc ggtgatagcc gactcaggct cctatttctg 750

cactgccaag ggccaggttg gctctgagca gcacagcgac attgtgaagt 800

ttgtggtcaa agactcctca aagctactca agaccaagac tgaggcacct 850

acaaccatga catacccctt gaaagcaaca tctacagtga agcagtcctg 900

ggactggacc actgacatgg atggctacct tggagagacc agtgctgggc 950

caggaaagag cctgcctgtc tttgccatca tcctcatcat ctccttgtgc 1000

tgtatggtgg tttttaccat ggcctatatc atgctctgtc ggaagacatc 1050

ccaacaagag catgtctacg aagcagccag gtaagaaagt ctctcctctt 1100

ccatttttga ccccgtccct gccctcaatt ttgattactg gcaggaaatg 1150

tggaggaagg ggggtgtggc acagacccaa tcctaaggcc ggaggccttc 1200

agggtcagga catagctgcc ttccctctct caggcacctt ctgaggttgt 1250

tttggccctc tgaacacaaa ggataattta gatccatctg ccttctgctt 1300

ccagaatccc tgggtggtag gatcctgata attaattggc aagaattgag 1350

gcagaagggt gggaaaccag gaccacagcc ccaagtccct tcttatgggt 1400

ggtgggctct tgggccatag ggcacatgcc agagaggcca acgactctgg 1450

agaaaccatg agggtggcca tcttcgcaag tggctgctcc agtgatgagc 1500

caacttccca gaatctgggc aacaactact ctgatgagcc ctgcatagga 1550

caggagtacc agatcatcgc ccagatcaat ggcaactacg cccgcctgct 1600

ggacacagtt cctctggatt atgagtttct ggccactgag ggcaaaagtg 1650

tctgttaaaa atgccccatt aggccaggat ctgctgacat aattgcctag 1700

tcagtccttg ccttctgcat ggccttcttc cctgctacct ctcttcctgg 1750

atagcccaaa gtgtccgcct accaacactg gagccgctgg gagtcactgg 1800

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ctttgccctg gaatttgcca gatgcatctc aagtaagcca gctgctggat 1850

ttggctctgg gcccttctag tatctctgcc gggggcttct ggtactcctc 1900

tctaaatacc agagggaaga tgcccatagc actaggactt ggtcatcatg 1950

cctacagaca ctattcaact ttggcatctt gccaccagaa gacccgaggg 2000

aggctcagct ctgccagctc agaggaccag ctatatccag gatcatttct 2050

ctttcttcag ggccagacag cttttaattg aaattgttat ttcacaggcc 2100

agggttcagt tctgctcctc cactataagt ctaatgttct gactctctcc 2150

tggtgctcaa taaatatcta atcataacag c 2181
```

```
<210> 52
<211> 321
<212> PRT
<213> Homo sapiens

<400> 52
Met Gly Ile Leu Leu Gly Leu Leu Leu Leu Gly His Leu Thr Val
 1               5                  10                  15

Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr
                20                  25                  30

Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro
                35                  40                  45

Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg
                50                  55                  60

Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp
                65                  70                  75

His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His
                80                  85                  90

Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met
                95                 100                 105

Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro
               110                 115                 120

Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val
               125                 130                 135

Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly
               140                 145                 150

Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys
               155                 160                 165

Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln
               170                 175                 180
```

```
Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr Leu Ser Thr
                185                 190                 195

Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser Tyr Phe
                200                 205                 210

Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp Ile
                215                 220                 225

Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys
                230                 235                 240

Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser
                245                 250                 255

Thr Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr
                260                 265                 270

Leu Gly Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe
                275                 280                 285

Ala Ile Ile Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr
                290                 295                 300

Met Ala Tyr Ile Met Leu Cys Arg Lys Thr Ser Gln Gln Glu His
                305                 310                 315

Val Tyr Glu Ala Ala Arg
                320
```

<210> 53
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 53
tatccctcca attgagcacc ctgg 24

<210> 54
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 54
gtcggaagac atcccaacaa g 21

<210> 55
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 55
cttcacaatg tcgctgtgct gctc 24

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 56
agccaaatcc agcagctggc ttac 24

<210> 57
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 57
tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58
<211> 2458
<212> DNA
<213> Homo sapiens

<400> 58
gcgccgggag cccatctgcc cccaggggca cggggcgcgg ggccggctcc 50

cgcccggcac atggctgcag ccacctcgcg cgcaccccga ggcgccgcgc 100

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agcaactgag cggggaagcg cccgcgtccg gggatcggga tgtccctcct 200

ccttctcctc ttgctagttt cctactatgt tggaaccttg gggactcaca 250

ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300

caactggggc ttccagaaaa agacactctg gatattgaat ggctgctcac 350

cgataatgaa gggaaccaaa aagtggtgat cacttactcc agtcgtcatg 400

tctacaataa cttgactgag gaacagaagg gccgagtggc ctttgcttcc 450

aatttcctgg caggagatgc ctccttgcag attgaacctc tgaagcccag 500

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tgcgagtaac tgtacagtat gtacaaagca tcggcatggt tgcaggagca 900

gtgacaggca tagtggctgg agccctgctg attttcctct tggtgtggct 950

gctaatccga aggaaagaca aagaaagata tgaggaagaa gagagaccta 1000

atgaaattcg agaagatgct gaagctccaa aagcccgtct tgtgaaaccc 1050

agctcctctt cctcaggctc tcggagctca cgctctggtt cttcctccac 1100

tcgctccaca gcaaatagtg cctcacgcag ccagcggaca ctgtcaactg 1150

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caaagcagaa accacaccca gcatgatccc cagccagagc agagccttcc 1300

aaacggtctg aattacaatg gacttgactc ccacgctttc ctaggagtca 1350

gggtctttgg actcttctcg tcattggagc tcaagtcacc agccacacaa 1400

ccagatgaga ggtcatctaa gtagcagtga gcattgcacg gaacagattc 1450

agatgagcat ttccttatac caataccaaa caagcaaaag gatgtaagct 1500

gattcatctg taaaaaggca tcttattgtg cctttagacc agagtaaggg 1550

aaagcaggag tccaaatcta tttgttgacc aggacctgtg gtgagaaggt 1600

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gtatcagtgc tttgattcac aattttcaag aggaaatggg atgctgtttg 1700

taaattttct atgcatttct gcaaacttat tggattatta gttattcaga 1750

cagtcaagca gaacccacag ccttattaca cctgtctaca ccatgtactg 1800

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ttgaaatagt gggagatgga gaagagtgaa tgagtttctc ccactctata 1950

ctaatctcac tatttgtatt gagcccaaaa taactatgaa aggagacaaa 2000

aatttgtgac aaaggattgt gaagagcttt ccatcttcat gatgttatga 2050

ggattgttga caaacattag aaatatataa tggagcaatt gtggatttcc 2100

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cctcaaatca gatgcctcta aggactttcc tgctagatat ttctggaagg 2150

agaaaataca acatgtcatt tatcaacgtc cttagaaaga attcttctag 2200

agaaaaaggg atctaggaat gctgaaagat tacccaacat accattatag 2250

tctcttcttt ctgagaaaat gtgaaaccag aattgcaaga ctgggtggac 2300

tagaaaggga gattagatca gttttctctt aatatgtcaa ggaaggtagc 2350

cgggcatggt gccaggcacc tgtaggaaaa tccagcaggt ggaggttgca 2400

gtgagccgag attatgccat tgcactccag cctgggtgac agagcgggac 2450

tccgtctc 2458

<210> 59
<211> 373
<212> PRT
<213> Homo sapiens

<400> 59
Met Ser Leu Leu Leu Leu Leu Leu Leu Val Ser Tyr Tyr Val Gly
 1               5                  10                  15

Thr Leu Gly Thr His Thr Glu Ile Lys Arg Val Ala Glu Glu Lys
                20                  25                  30

Val Thr Leu Pro Cys His His Gln Leu Gly Leu Pro Glu Lys Asp
                35                  40                  45

Thr Leu Asp Ile Glu Trp Leu Leu Thr Asp Asn Glu Gly Asn Gln
                50                  55                  60

Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu
                65                  70                  75

Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu
                80                  85                  90

Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp
                95                 100                 105

Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val
               110                 115                 120

Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro
               125                 130                 135

Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr
               140                 145                 150

Leu Gln Cys Glu Ser Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr
               155                 160                 165

Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro
               170                 175                 180
```

```
Pro Lys Ser Arg Ile Asp Tyr Asn His Pro Gly Arg Val Leu Leu
                185                 190                 195

Gln Asn Leu Thr Met Ser Tyr Ser Gly Leu Tyr Gln Cys Thr Ala
                200                 205                 210

Gly Asn Glu Ala Gly Lys Glu Ser Cys Val Val Arg Val Thr Val
                215                 220                 225

Gln Tyr Val Gln Ser Ile Gly Met Val Ala Gly Ala Val Thr Gly
                230                 235                 240

Ile Val Ala Gly Ala Leu Leu Ile Phe Leu Leu Val Trp Leu Leu
                245                 250                 255

Ile Arg Arg Lys Asp Lys Glu Arg Tyr Glu Glu Glu Glu Arg Pro
                260                 265                 270

Asn Glu Ile Arg Glu Asp Ala Glu Ala Pro Lys Ala Arg Leu Val
                275                 280                 285

Lys Pro Ser Ser Ser Ser Ser Gly Ser Arg Ser Ser Arg Ser Gly
                290                 295                 300

Ser Ser Ser Thr Arg Ser Thr Ala Asn Ser Ala Ser Arg Ser Gln
                305                 310                 315

Arg Thr Leu Ser Thr Asp Ala Ala Pro Gln Pro Gly Leu Ala Thr
                320                 325                 330

Gln Ala Tyr Ser Leu Val Gly Pro Glu Val Arg Gly Ser Glu Pro
                335                 340                 345

Lys Lys Val His His Ala Asn Leu Thr Lys Ala Glu Thr Thr Pro
                350                 355                 360

Ser Met Ile Pro Ser Gln Ser Arg Ala Phe Gln Thr Val
                365                 370
```

<210> 60
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 60
ccagtgcaca gcaggcaacg aagc 24

<210> 61
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 61
actaggctgt atgcctgggt gggc 24

<210> 62
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 62
gtatgtacaa agcatcggca tggttgcagg agcagtgaca ggc 43

<210> 63
<211> 3534
<212> DNA
<213> Homo sapiens

<400> 63
gtcgttcctt tgctctctcg cgcccagtcc tcctccctgg ttctcctcag 50

ccgctgtcgg aggagagcac ccggagacgc gggctgcagt cgcggcggct 100

tctccccgcc tgggcggcct cgccgctggg caggtgctga gcgcccctag 150

agcctccctt gccgcctccc tcctctgccc ggccgcagca gtgcacatgg 200

ggtgttggag gtagatgggc tcccggcccg ggaggcggcg gtggatgcgg 250

cgctgggcag aagcagccgc cgattccagc tgccccgcgc gccccgggcg 300

cccctgcgag tccccggttc agccatgggg acctctccga gcagcagcac 350

cgccctcgcc tcctgcagcc gcatcgcccg ccgagccaca gccacgatga 400

tcgcgggctc ccttctcctg cttggattcc ttagcaccac cacagctcag 450

ccagaacaga aggcctcgaa tctcattggc acataccgcc atgttgaccg 500

tgccaccggc caggtgctaa cctgtgacaa gtgtccagca ggaacctatg 550

tctctgagca ttgtaccaac acaagcctgc gcgtctgcag cagttgccct 600

gtggggacct ttaccaggca tgagaatggc atagagaaat gccatgactg 650

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ctgacaacac aagctcagca agggggaagg aagacgtgaa caagaccctc 1200

ccaaaccttc aggtagtcaa ccaccagcaa ggcccccacc acagacacat 1250

cctgaagctg ctgccgtcca tggaggccac tgggggcgag aagtccagca 1300

cgcccatcaa gggccccaag aggggacatc ctagacagaa cctacacaag 1350

cattttgaca tcaatgagca tttgccctgg atgattgtgc ttttcctgct 1400

gctggtgctt gtggtgattg tggtgtgcag tatccggaaa agctcgagga 1450

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aagattcgtg ggctgatgga agacaccacc cagctggaaa ctgacaaact 1850

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gtagtggtga aggaccgata tcagaaaaat gccttcaagt gtactaattt 3500

attaataaac attaggtgtt tgttaaaaaa aaaa 3534

<210> 64
<211> 655
<212> PRT
<213> Homo sapiens

<400> 64
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1   5   10   15

Arg Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu
                20   25   30

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Leu Leu Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln
                35                  40                  45

Lys Ala Ser Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala
                50                  55                  60

Thr Gly Gln Val Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr
                65                  70                  75

Val Ser Glu His Cys Thr Asn Thr Ser Leu Arg Val Cys Ser Ser
                80                  85                  90

Cys Pro Val Gly Thr Phe Thr Arg His Glu Asn Gly Ile Glu Lys
                95                  100                 105

Cys His Asp Cys Ser Gln Pro Cys Pro Trp Pro Met Ile Glu Lys
                110                 115                 120

Leu Pro Cys Ala Ala Leu Thr Asp Arg Glu Cys Thr Cys Pro Pro
                125                 130                 135

Gly Met Phe Gln Ser Asn Ala Thr Cys Ala Pro His Thr Val Cys
                140                 145                 150

Pro Val Gly Trp Gly Val Arg Lys Lys Gly Thr Glu Thr Glu Asp
                155                 160                 165

Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe Ser Asp Val Pro
                170                 175                 180

Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys Leu Ser Gln
                185                 190                 195

Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp Asn Val
                200                 205                 210

Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser Pro
                215                 220                 225

Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu
                230                 235                 240

Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu
                245                 250                 255

Ser Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile
                260                 265                 270

Gln Glu Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys
                275                 280                 285

Glu Asp Val Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His
                290                 295                 300

Gln Gln Gly Pro His His Arg His Ile Leu Lys Leu Leu Pro Ser
                305                 310                 315

Met Glu Ala Thr Gly Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly
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320 325 330

Pro Lys Arg Gly His Pro Arg Gln Asn Leu His Lys His Phe Asp
335 340 345

Ile Asn Glu His Leu Pro Trp Met Ile Val Leu Phe Leu Leu Leu
350 355 360

Val Leu Val Val Ile Val Val Cys Ser Ile Arg Lys Ser Ser Arg
365 370 375

Thr Leu Lys Lys Gly Pro Arg Gln Asp Pro Ser Ala Ile Val Glu
380 385 390

Lys Ala Gly Leu Lys Lys Ser Met Thr Pro Thr Gln Asn Arg Glu
395 400 405

Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile Asp Ile Leu Lys
410 415 420

Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln
425 430 435

Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe Ser Asn
440 445 450

Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln His
455 460 465

Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser
470 475 480

Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg
485 490 495

Gly Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala
500 505 510

Leu Pro Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser
515 520 525

Pro Asn Ala Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro
530 535 540

Ser Pro Gln Asp Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu
545 550 555

Pro Leu Leu Arg Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu
560 565 570

Ser Arg Asn Gly Ser Phe Ile Thr Lys Glu Lys Lys Asp Thr Val
575 580 585

Leu Arg Gln Val Arg Leu Asp Pro Cys Asp Leu Gln Pro Ile Phe
590 595 600

Asp Asp Met Leu His Phe Leu Asn Pro Glu Glu Leu Arg Val Ile
605 610 615

Glu Glu Ile Pro Gln Ala Glu Asp Lys Leu Asp Arg Leu Phe Glu
620 625 630

Ile Ile Gly Val Lys Ser Gln Glu Ala Ser Gln Thr Leu Leu Asp
635 640 645

Ser Val Tyr Ser His Leu Pro Asp Leu Leu
650 655

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 65
gtagcagtgc acatggggtg ttgg 24

<210> 66
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 66
accgcacatc ctcagtctct gtcc 24

<210> 67
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 67
acgatgatcg cgggctccct tctcctgctt ggattcctta gcaccaccac 50

<210> 68
<211> 2412
<212> DNA
<213> Homo sapiens

<400> 68
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acatttttgg gactcgggaa ttatgaggta gaggtggagg cggagccgga 100

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ttgaagcccc cttctcattc cgatcgcttt ttggccttga tgatttgaaa 200

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aagtacagat gtcgctcatc ctttaagtgt atcgagctga tagctcgatg 400

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cgtggacagc tgccaggggg acagcggggg gcccctggtg tgtcaagaga 1350

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ttccctcatt gtctggcgtg tctgcgtgga ctggtgacgt gaatcaaaat 2400

catccactga aa 2412

<210> 69
<211> 453
<212> PRT
<213> Homo sapiens

<400> 69

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Met Gly Glu Asn Asp Pro Pro Ala Val Glu Ala Pro Phe Ser Phe
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Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala
                20                  25                  30

Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro
                35                  40                  45

Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile
                50                  55                  60

Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly
                65                  70                  75

Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala
                80                  85                  90

Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr
                95                 100                 105

Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe
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110 115 120

Thr Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly
125 130 135

His Tyr Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr
140 145 150

Val Ser Ser Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe
155 160 165

Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys
170 175 180

Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu Gly Cys Ala
185 190 195

Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly His Arg
200 205 210

Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu Leu
215 220 225

Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His
230 235 240

Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala
245 250 255

Ala His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile
260 265 270

Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His
275 280 285

Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg
290 295 300

Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr
305 310 315

Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu Glu
320 325 330

Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala
335 340 345

Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala
350 355 360

Val Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr
365 370 375

Gly Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr
380 385 390

Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
395 400 405

```
 Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe
                 410                 415                 420

 Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg
                 425                 430                 435

 Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp
                 440                 445                 450

 Leu Lys Thr


<210> 70
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 70
 tgacatcgcc cttatgaagc tggc 24

<210> 71
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 71
 tacacgtccc tgtggttgca gatc 24

<210> 72
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 72
 cgttcaatgc agaaatgatc cagcctgtgt gcctgcccaa ctctgaagag 50

<210> 73
<211> 3305
<212> DNA
<213> Homo sapiens

<400> 73
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 attgcaacgg tcaaggctgg cttgtgccag aacggcgcgc gcgcgcgcac 100

 gcacgcacac acacgggggg aaactttttt aaaaatgaaa ggctagaaga 150

 gctcagcggc ggcgcgggcg ctgcgcgagg gctccggagc tgactcgccg 200
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ataaatctgg aaagaaatga aggtctcatt gccagcagtt tcacggaaac 600

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gtcactgtta ctaccatgga catgtacggg gatattctga ttcagcagtc 700

agtctcagca cgtgttctgg tctcagggga cttattgtgt ttgaaaatga 750

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agtactcagg tttgagggtt tgcagaaagc cagggaaccc acagagtcac 3200

caacccttca tttaacaagt aagaatgtta aaaagtgaaa acaatgtaag 3250

agcctaactc catcccccgt ggccattact gcataaaata gagtgcattt 3300

gaaat 3305

<210> 74
<211> 735
<212> PRT
<213> Homo sapiens

<400> 74
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Leu Ala Leu Ala Gly Ala Leu Leu Ala Pro Cys Glu Ala Arg Gly
                 20                  25                  30

Val Ser Leu Trp Asn Gln Gly Arg Ala Asp Glu Val Val Ser Ala
                 35                  40                  45

Ser Val Arg Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp
                 50                  55                  60

Ser Lys Asn His Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu
                 65                  70                  75

Ser Lys Glu Leu Ile Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile
                 80                  85                  90

Ala Ser Ser Phe Thr Glu Thr His Tyr Leu Gln Asp Gly Thr Asp
                 95                 100                 105

Val Ser Leu Ala Arg Asn Tyr Thr Gly His Cys Tyr Tyr His Gly
                110                 115                 120

His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys
                125                 130                 135

Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val
                140                 145                 150

Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro
                155                 160                 165

Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His
                170                 175                 180

Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser
                185                 190                 195

Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr
                200                 205                 210
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Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln
215 220 225

Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu
230 235 240

Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg
245 250 255

Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys
260 265 270

Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp
275 280 285

Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala
290 295 300

Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met
305 310 315

Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile
320 325 330

Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu
335 340 345

Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu
350 355 360

Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys
365 370 375

Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser
380 385 390

Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met
395 400 405

Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly
410 415 420

Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Gly Glu Glu Cys
425 430 435

Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys Asn Ala
440 445 450

Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly Leu
455 460 465

Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr Ala Cys Arg
470 475 480

Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala
485 490 495

Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His Ser

500 505 510

Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr
515 520 525

His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro
530 535 540

Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro
545 550 555

Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys
560 565 570

Glu Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly
575 580 585

Ala Ser Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr
590 595 600

Asn Ile Pro Leu Gln Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr
605 610 615

His Val Tyr Leu Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu
620 625 630

Ala Gly Thr Lys Cys Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln
635 640 645

Cys Gln Asn Ile Ser Val Phe Gly Val His Glu Cys Ala Met Gln
650 655 660

Cys His Gly Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys
665 670 675

Glu Ala His Trp Ala Pro Pro Phe Cys Asp Lys Phe Gly Phe Gly
680 685 690

Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala Glu Ala Arg Gln
695 700 705

Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly Gln Glu Pro
710 715 720

Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr Leu Ile
725 730 735

<210> 75
<211> 483
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473
<223> unknown base

<400> 75

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ctacccagga agtttgcaga aacagtgcaa ggaagggcag ganttcctgg 150

ttgagntttt tgntaaaaca tggacatgnt tcagtgctgc tcntgagaga 200

gtagcaggtt accacttttg gcaggcccca gccctgcagc aaggaggaag 250

aggactcaaa agtttggcct ttcactgagc ctccacagca gtgggggaga 300

agcaagggtt gggcccagtg tcccctttcc ccagtgacac ctcagccttg 350

gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400

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gagaccctgc cacccattcc atntccatcc aag 483

<210> 76
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<223> Synthetic oligonucleotide probe

<400> 76
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<210> 77
<211> 18
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 77
catgagcatg tgcacggc 18

<210> 78
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<400> 78
tacctgcacg atgggcac 18

<210> 79
<211> 18
<212> DNA
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<220>
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<400> 79
cactgggcac ctcccttc 18

<210> 80
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 80
ctccaggctg gtctccaagt ccttcc 26

<210> 81
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
tccctgttgg actctgcagc ttcc 24

<210> 82
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 82
cttcgctggg aagagtttg 19

<210> 83
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 83
gtgcaaccaa cagatacaaa ctcttcccag cgaagaagct gaaaagcgtc 50

<210> 84
<211> 1714
<212> DNA
<213> Homo sapiens

<400> 84
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<210> 85
<211> 67
<212> PRT
<213> Homo sapiens

<400> 85
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Met Gly Lys Gly Met Val Ala Met Leu Ile Leu Gly Leu Leu Leu
  1               5                  10                  15

Leu Ala Leu Leu Leu Pro Val Gln Val Ser Ser Phe Val Pro Leu
                 20                  25                  30

Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser
                 35                  40                  45

Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu
                 50                  55                  60

Ala Leu Leu His Leu Tyr His
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<210> 86
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 86
acgggcacac tggatcccaa atg 23

<210> 87
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 87
ggtagagatg tagaagggca agcaagacc 29

<210> 88
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 88
gctccctacc cgtgcaggtt tcttcatttg ttcctttaac cagtatgccg 50

<210> 89
<211> 2956
<212> DNA
<213> Homo sapiens

<400> 89
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gctgctgctg ggccatggcg gcggcgggcg ctggggcgcc cgggcccagg 150

aggcggcggc ggcggcggcg gacgggcccc ccgcggcaga cggcgaggac 200

ggacaggacc cgcacagcaa gcacctgtac acggccgaca tgttcacgca 250

cgggatccag agcgccgcgc acttcgtcat gttcttcgcg ccctggtgtg 300

gacactgcca gcggctgcag ccgacttgga atgacctggg agacaaatac 350

aacagcatgg aagatgccaa agtctatgtg gctaaagtgg actgcacggc 400

ccactccgac gtgtgctccg cccagggggt gcgaggatac cccaccttaa 450

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tgcatccaac actcttcacc cacctcccat acgcaagggg atgtggatac 2650

ttggcccaaa gtaactggtg gtaggaatct tagaaacaag accacttata 2700

ctgtctgtct gaggcagaag ataacagcag catctcgacc agcctctgcc 2750

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ggtacaattt gtttgtttac actatgatac tttctaaata aactcttttt 2950

ttttaa 2956

<210> 90
<211> 432
<212> PRT
<213> Homo sapiens

<400> 90
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Ala Ala Leu Thr Ala Leu Leu Leu Leu Leu Leu Gly His Gly Gly
20 25 30

Gly Gly Arg Trp Gly Ala Arg Ala Gln Glu Ala Ala Ala Ala Ala
35 40 45

Ala Asp Gly Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro
50 55 60

His Ser Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile
65 70 75

Gln Ser Ala Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly
80 85 90

His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys
95 100 105

Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp
110 115 120

Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly
125 130 135

Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys
140 145 150

Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu
155 160 165

Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu
170 175 180

```
Pro Pro Ser Ala Pro Glu Leu Lys Gln Gly Leu Tyr Glu Leu Ser
                185                 190                 195

Ala Ser Asn Phe Glu Leu His Val Ala Gln Gly Asp His Phe Ile
                200                 205                 210

Lys Phe Phe Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro
                215                 220                 225

Thr Trp Glu Gln Leu Ala Leu Gly Leu Glu His Ser Glu Thr Val
                230                 235                 240

Lys Ile Gly Lys Val Asp Cys Thr Gln His Tyr Glu Leu Cys Ser
                245                 250                 255

Gly Asn Gln Val Arg Gly Tyr Pro Thr Leu Leu Trp Phe Arg Asp
                260                 265                 270

Gly Lys Lys Val Asp Gln Tyr Lys Gly Lys Arg Asp Leu Glu Ser
                275                 280                 285

Leu Arg Glu Tyr Val Glu Ser Gln Leu Gln Arg Thr Glu Thr Gly
                290                 295                 300

Ala Thr Glu Thr Val Thr Pro Ser Glu Ala Pro Val Leu Ala Ala
                305                 310                 315

Glu Pro Glu Ala Asp Lys Gly Thr Val Leu Ala Leu Thr Glu Asn
                320                 325                 330

Asn Phe Asp Asp Thr Ile Ala Glu Gly Ile Thr Phe Ile Lys Phe
                335                 340                 345

Tyr Ala Pro Trp Cys Gly His Cys Lys Thr Leu Ala Pro Thr Trp
                350                 355                 360

Glu Glu Leu Ser Lys Lys Glu Phe Pro Gly Leu Ala Gly Val Lys
                365                 370                 375

Ile Ala Glu Val Asp Cys Thr Ala Glu Arg Asn Ile Cys Ser Lys
                380                 385                 390

Tyr Ser Val Arg Gly Tyr Pro Thr Leu Leu Leu Phe Arg Gly Gly
                395                 400                 405

Lys Lys Val Ser Glu His Ser Gly Gly Arg Asp Leu Asp Ser Leu
                410                 415                 420

His Arg Phe Val Leu Ser Gln Ala Lys Asp Glu Leu
                425                 430
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<210> 91
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 91
atgttcttcg cgccctggtg 20

<210> 92
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 92
ccaagccaac acactctaca g 21

<210> 93
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 93
aagtggtcgc cttgtgcaac gtgc 24

<210> 94
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 94
ggtcaaaggg gatatatcgc cac 23

<210> 95
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 95
gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggccca 49

<210> 96
<211> 1016
<212> DNA
<213> Homo sapiens

<400> 96
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aaaccaattt atcctcctgg tactatttct tttgcaaatt cagagtctgg 100

gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150 atttcaccag gacccaaagg agatgatggt gaaaaaggag atccaggaga 200

agagggaaag catggcaaag tgggacgcat ggggccgaaa ggaattaaag 250

gagaactggg tgatatggga gatcagggca atattggcaa gactgggccc 300

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aaaaaaaaaa aaaaaa 1016

<210> 97
<211> 277
<212> PRT
<213> Homo sapiens

<400> 97
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                20                  25                  30

Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser
                35                  40                  45

Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu
                50                  55                  60

Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile
                65                  70                  75

Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys
```

```
                80                  85                  90

Thr Gly Pro Ile Gly Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu
                95                  100                 105

Leu Gly Ile Pro Gly Glu Lys Gly Lys Ala Gly Thr Val Cys Asp
                110                 115                 120

Cys Gly Arg Tyr Arg Lys Phe Val Gly Gln Leu Asp Ile Ser Ile
                125                 130                 135

Ala Arg Leu Lys Thr Ser Met Lys Phe Val Lys Asn Val Ile Ala
                140                 145                 150

Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr Tyr Ile Val Gln Glu
                155                 160                 165

Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys Arg Ile Arg Gly
                170                 175                 180

Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn Thr Leu Ile
                185                 190                 195

Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe Ile Gly
                200                 205                 210

Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Ser Thr Asp Asn
                215                 220                 225

Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser
                230                 235                 240

Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly
                245                 250                 255

Arg Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys
                260                 265                 270

Glu Phe Ile Lys Lys Lys Lys
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<210> 98
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 98
cgctgactat gttgccaaga gtgg 24

<210> 99
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 99
gatgatggag gctccatacc tcag 24

<210> 100
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 100
gtgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101
<211> 2574
<212> DNA
<213> Homo sapiens

<400> 101
ggttctatcg attcgaattc ggccacactg gccggatcct ctagagatcc 50

ctcgacctcg acccacgcgt ccgctgctct ccgcccgtgt ggagtggtgg 100

gggcctgggt gggaatgggc gtgtgccagc gcacgcgcgc tccctggaag 150

gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200

agggatgttt gcgagcggct ggaaccagac ggtgccgata gaggaagcgg 250

gctccatggc tgccctcctg ctgctgcccc tgctgctgtt gctaccgctg 300

ctgctgctga agctacacct ctggccgcag ttgcgctggc ttccggcgga 350

cttggccttt gcggtgcgag ctctgtgctg caaaagggct cttcgagctc 400

gcgccctggc cgcggctgcc gccgacccgg aaggtcccga gggggctgc 450

agcctggcct ggcgcctcgc ggaactggcc cagcagcgcg ccgcgcacac 500

ctttctcatt cacggctcgc ggcgctttag ctactcagag gcggagcgcg 550

agagtaacag ggctgcacgc gccttcctac gtgcgctagg ctgggactgg 600

ggacccgacg gcggcgacag cggcgagggg agcgctggag aaggcgagcg 650

ggcagcgccg ggagccggag atgcagcggc cggaagcggc gcggagtttg 700

ccggagggga cggtgccgcc agaggtggag gagccgccgc ccctctgtca 750

cctggagcaa ctgtggcgct gctcctcccc gctggcccag agtttctgtg 800

gctctggttc gggctggcca aggccggcct gcgcactgcc tttgtgccca 850

ccgccctgcg ccggggcccc ctgctgcact gcctccgcag ctgcggcgcg 900 cgcgcgctgg tgctggcgcc agagtttctg gagtccctgg agccggacct 950

gcccgccctg agagccatgg ggctccacct gtgggctgca ggcccaggaa 1000

cccaccctgc tggaattagc gatttgctgg ctgaagtgtc cgctgaagtg 1050

gatgggccag tgccaggata cctctcttcc ccccagagca taacagacac 1100

gtgcctgtac atcttcacct ctggcaccac gggcctcccc aaggctgctc 1150

ggatcagtca tctgaagatc ctgcaatgcc agggcttcta tcagctgtgt 1200

ggtgtccacc aggaagatgt gatctacctc gccctcccac tctaccacat 1250

gtccggttcc ctgctgggca tcgtgggctg catgggcatt ggggccacag 1300

tggtgctgaa atccaagttc tcggctggtc agttctggga agattgccag 1350

cagcacaggg tgacggtgtt ccagtacatt ggggagctgt gccgatacct 1400

tgtcaaccag cccccgagca aggcagaacg tggccataag gtccggctgg 1450

cagtgggcag cgggctgcgc ccagatacct gggagcgttt tgtgcggcgc 1500

ttcgggcccc tgcaggtgct ggagacatat ggactgacag agggcaacgt 1550

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acaggagagc caattcggga cccccagggg cactgtatgg ccacatctcc 1700

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tgggctatgc tggcgggcca gagctggccc aggggaagtt gctaaaggat 1800

gtcttccggc ctggggatgt tttcttcaac actggggacc tgctggtctg 1850

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ggtggaaggg ggagaatgtg gccacaaccg aggtggcaga ggtcttcgag 1950

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gcaccctgtc tgacccactg tacgttctgg accaggctgt aggtgcctac 2250

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aatctgagaa cttccacacc tgaggcacct gagagaggaa ctctgtgggg 2350

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tgggggccgt tgcaggtgta ctgggctgtc agggatcttt tctataccag 2400

aactgcggtc actattttgt aataaatgtg gctggagctg atccagctgt 2450

ctctgaccta aaaaaaaaaa aaaaaaaaaa aaaaaaaaag ggcggccgcg 2500

actctagagt cgacctgcag tagggataac agggtaataa gcttggccgc 2550

catggcccaa cttgtttatt gcag 2574

<210> 102
<211> 730
<212> PRT
<213> Homo sapiens

<400> 102
Met Gly Val Cys Gln Arg Thr Arg Ala Pro Trp Lys Glu Lys Ser
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Gln Leu Glu Arg Ala Ala Leu Gly Phe Arg Lys Gly Gly Ser Gly
                20                  25                  30

Met Phe Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala
                35                  40                  45

Gly Ser Met Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu
                50                  55                  60

Pro Leu Leu Leu Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp
                65                  70                  75

Leu Pro Ala Asp Leu Ala Phe Ala Val Arg Ala Leu Cys Cys Lys
                80                  85                  90

Arg Ala Leu Arg Ala Arg Ala Leu Ala Ala Ala Ala Ala Asp Pro
                95                 100                 105

Glu Gly Pro Glu Gly Gly Cys Ser Leu Ala Trp Arg Leu Ala Glu
               110                 115                 120

Leu Ala Gln Gln Arg Ala Ala His Thr Phe Leu Ile His Gly Ser
               125                 130                 135

Arg Arg Phe Ser Tyr Ser Glu Ala Glu Arg Glu Ser Asn Arg Ala
               140                 145                 150

Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp Asp Trp Gly Pro Asp
               155                 160                 165

Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu Gly Glu Arg Ala
               170                 175                 180

Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly Ala Glu Phe
               185                 190                 195

Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala Ala Pro
               200                 205                 210
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Leu Ser Pro Gly Ala Thr Val Ala Leu Leu Leu Pro Ala Gly Pro
215 220 225

Glu Phe Leu Trp Leu Trp Phe Gly Leu Ala Lys Ala Gly Leu Arg
230 235 240

Thr Ala Phe Val Pro Thr Ala Leu Arg Arg Gly Pro Leu Leu His
245 250 255

Cys Leu Arg Ser Cys Gly Ala Arg Ala Leu Val Leu Ala Pro Glu
260 265 270

Phe Leu Glu Ser Leu Glu Pro Asp Leu Pro Ala Leu Arg Ala Met
275 280 285

Gly Leu His Leu Trp Ala Ala Gly Pro Gly Thr His Pro Ala Gly
290 295 300

Ile Ser Asp Leu Leu Ala Glu Val Ser Ala Glu Val Asp Gly Pro
305 310 315

Val Pro Gly Tyr Leu Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys
320 325 330

Leu Tyr Ile Phe Thr Ser Gly Thr Thr Gly Leu Pro Lys Ala Ala
335 340 345

Arg Ile Ser His Leu Lys Ile Leu Gln Cys Gln Gly Phe Tyr Gln
350 355 360

Leu Cys Gly Val His Gln Glu Asp Val Ile Tyr Leu Ala Leu Pro
365 370 375

Leu Tyr His Met Ser Gly Ser Leu Leu Gly Ile Val Gly Cys Met
380 385 390

Gly Ile Gly Ala Thr Val Val Leu Lys Ser Lys Phe Ser Ala Gly
395 400 405

Gln Phe Trp Glu Asp Cys Gln Gln His Arg Val Thr Val Phe Gln
410 415 420

Tyr Ile Gly Glu Leu Cys Arg Tyr Leu Val Asn Gln Pro Pro Ser
425 430 435

Lys Ala Glu Arg Gly His Lys Val Arg Leu Ala Val Gly Ser Gly
440 445 450

Leu Arg Pro Asp Thr Trp Glu Arg Phe Val Arg Arg Phe Gly Pro
455 460 465

Leu Gln Val Leu Glu Thr Tyr Gly Leu Thr Glu Gly Asn Val Ala
470 475 480

Thr Ile Asn Tyr Thr Gly Gln Arg Gly Ala Val Gly Arg Ala Ser
485 490 495

Trp Leu Tyr Lys His Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp

500 505 510

Val Thr Thr Gly Glu Pro Ile Arg Asp Pro Gln Gly His Cys Met
515 520 525

Ala Thr Ser Pro Gly Glu Pro Gly Leu Leu Val Ala Pro Val Ser
530 535 540

Gln Gln Ser Pro Phe Leu Gly Tyr Ala Gly Gly Pro Glu Leu Ala
545 550 555

Gln Gly Lys Leu Leu Lys Asp Val Phe Arg Pro Gly Asp Val Phe
560 565 570

Phe Asn Thr Gly Asp Leu Leu Val Cys Asp Asp Gln Gly Phe Leu
575 580 585

Arg Phe His Asp Arg Thr Gly Asp Thr Phe Arg Trp Lys Gly Glu
590 595 600

Asn Val Ala Thr Thr Glu Val Ala Glu Val Phe Glu Ala Leu Asp
605 610 615

Phe Leu Gln Glu Val Asn Val Tyr Gly Val Thr Val Pro Gly His
620 625 630

Glu Gly Arg Ala Gly Met Ala Ala Leu Val Leu Arg Pro Pro His
635 640 645

Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val Ser Glu Asn Leu
650 655 660

Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln Glu Ser Leu
665 670 675

Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met Ala Asn
680 685 690

Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val Leu
695 700 705

Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr
710 715 720

Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile
725 730

<210> 103
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 103
gagagccatg gggctccacc tg 22

<210> 104
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 104
ggagaatgtg gccacaac 18

<210> 105
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 105
gccctggcac agtgactcca tagacg 26

<210> 106
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 106
atccacttca gcggacac 18

<210> 107
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 107
ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

<210> 108
<211> 2579
<212> DNA
<213> Homo sapiens

<400> 108
cctgtgttaa gctgaggttt cccctagatc tcgtatatcc ccaacacata 50

cctccacgca cacacatccc caagaacctc gagctcacac caacagacac 100

acgcgcgcat acacactcgc tctcgcttgt ccatctccct cccgggggag 150

ccggcgcgcg ctcccacctt tgccgcacac tccggcgagc cgagcccgca 200 gcgctccagg attctgcggc tcggaactcg gattgcagct ctgaaccccc 250

atggtggttt tttaaacact tcttttcctt ctcttcctcg ttttgattgc 300

accgtttcca tctgggggct agaggagcaa ggcagcagcc ttcccagcca 350

gcccttgttg gcttgccatc gtccatctgg cttataaaag tttgctgagc 400

gcagtccaga gggctgcgct gctcgtcccc tcggctggca gaagggggtg 450

acgctgggca gcggcgagga gcgcgccgct gcctctggcg ggctttcggc 500

ttgaggggca aggtgaagag cgcaccggcc gtggggttta ccgagctgga 550

tttgtatgtt gcaccatgcc ttcttggatc ggggctgtga ttcttcccct 600

cttggggctg ctgctctccc tccccgccgg ggcggatgtg aaggctcgga 650

gctgcggaga ggtccgccag gcgtacggtg ccaagggatt cagcctggcg 700

gacatcccct accaggagat cgcaggggaa cacttaagaa tctgtcctca 750

ggaatataca tgctgcacca cagaaatgga agacaagtta agccaacaaa 800

gcaaactcga atttgaaaac cttgtggaag agacaagcca ttttgtgcgc 850

accacttttg tgtccaggca taagaaattt gacgaatttt tccgagagct 900

cctggagaat gcagaaaagt cactaaatga tatgtttgta cggacctatg 950

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agtatcactt cagtgaagac tacctggaat gtgtgagcaa atacactgac 1150

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cgtgccctca tgaagatgct gtactgccca tactgtcggg ggcttcccac 1350

tgtgaggccc tgcaacaact actgtctcaa cgtcatgaag ggctgcttgg 1400

caaatcaggc tgacctcgac acagagtgga atctgtttat agatgcaatg 1450

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ggacccgata gatgtcaaga tttctgaagc cattatgaac atgcaagaaa 1550

acagcatgca ggtgtctgca aaggtctttc agggatgtgg tcagcccaaa 1600

cctgctccag ccctcagatc tgcccgctca gctcctgaaa atttaatac 1650 acgtttcagg ccctacaatc ctgaggaaag accaacaact gctgcaggca 1700

caagcttgga ccggctggtc acagacataa aagagaaatt gaagctctct 1750

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gacagcgggc acgtccaacg aggaggaatg ctggaacggg cacagcaaag 1850

ccagatactt gcctgagatc atgaatgatg ggctcaccaa ccagatcaac 1900

aatcccgagg tggatgtgga catcactcgg cctgacactt tcatcagaca 1950

gcagattatg gctctccgtg tgatgaccaa caaactaaaa aacgcctaca 2000

atggcaatga tgtcaatttc caggacacaa gtgatgaatc cagtggctca 2050

gggagtggca gtgggtgcat ggatgacgtg tgtcccacgg agtttgagtt 2100

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gatgaaactg cattttagct atctgaatgg ccaactcact tcttttctta 2300

cactcttgga caatggacca tgccacaaaa acttaccgtt ttctatgaga 2350

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gggtgccaga ctgaactgct tcctctttcc ttcagctatc tgtggggacc 2450

ttgtttattc tagagagaat tcttactcaa atttttcgta ccaggagatt 2500

ttcttacctt catttgcttt tatgctgcag aagtaaagga atctcacgtt 2550

gtgagggttt ttttttctc atttaaaat 2579

<210> 109
<211> 555
<212> PRT
<213> Homo sapiens

<400> 109
Met Pro Ser Trp Ile Gly Ala Val Ile Leu Pro Leu Leu Gly Leu
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Leu Leu Ser Leu Pro Ala Gly Ala Asp Val Lys Ala Arg Ser Cys
                20   25   30

Gly Glu Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala
                35   40   45

Asp Ile Pro Tyr Gln Glu Ile Ala Gly Glu His Leu Arg Ile Cys
                50   55   60

Pro Gln Glu Tyr Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu
                65   70   75

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Ser Gln Gln Ser Lys Leu Glu Phe Glu Asn Leu Val Glu Glu Thr
                80                  85                  90

Ser His Phe Val Arg Thr Thr Phe Val Ser Arg His Lys Lys Phe
                95                  100                 105

Asp Glu Phe Phe Arg Glu Leu Leu Glu Asn Ala Glu Lys Ser Leu
                110                 115                 120

Asn Asp Met Phe Val Arg Thr Tyr Gly Met Leu Tyr Met Gln Asn
                125                 130                 135

Ser Glu Val Phe Gln Asp Leu Phe Thr Glu Leu Lys Arg Tyr Tyr
                140                 145                 150

Thr Gly Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp
                155                 160                 165

Ala Arg Leu Leu Glu Arg Met Phe Gln Leu Ile Asn Pro Gln Tyr
                170                 175                 180

His Phe Ser Glu Asp Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp
                185                 190                 195

Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Ile Gln
                200                 205                 210

Val Thr Arg Ala Phe Ile Ala Ala Arg Thr Phe Val Gln Gly Leu
                215                 220                 225

Thr Val Gly Arg Glu Val Ala Asn Arg Val Ser Lys Val Ser Pro
                230                 235                 240

Thr Pro Gly Cys Ile Arg Ala Leu Met Lys Met Leu Tyr Cys Pro
                245                 250                 255

Tyr Cys Arg Gly Leu Pro Thr Val Arg Pro Cys Asn Asn Tyr Cys
                260                 265                 270

Leu Asn Val Met Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp
                275                 280                 285

Thr Glu Trp Asn Leu Phe Ile Asp Ala Met Leu Leu Val Ala Glu
                290                 295                 300

Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile
                305                 310                 315

Asp Val Lys Ile Ser Glu Ala Ile Met Asn Met Gln Glu Asn Ser
                320                 325                 330

Met Gln Val Ser Ala Lys Val Phe Gln Gly Cys Gly Gln Pro Lys
                335                 340                 345

Pro Ala Pro Ala Leu Arg Ser Ala Arg Ser Ala Pro Glu Asn Phe
                350                 355                 360

Asn Thr Arg Phe Arg Pro Tyr Asn Pro Glu Glu Arg Pro Thr Thr
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                365                 370                 375

Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu
                380                 385                 390

Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr
                395                 400                 405

Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu
                410                 415                 420

Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile
                425                 430                 435

Met Asn Asp Gly Leu Thr Asn Gln Ile Asn Asn Pro Glu Val Asp
                440                 445                 450

Val Asp Ile Thr Arg Pro Asp Thr Phe Ile Arg Gln Gln Ile Met
                455                 460                 465

Ala Leu Arg Val Met Thr Asn Lys Leu Lys Asn Ala Tyr Asn Gly
                470                 475                 480

Asn Asp Val Asn Phe Gln Asp Thr Ser Asp Glu Ser Ser Gly Ser
                485                 490                 495

Gly Ser Gly Ser Gly Cys Met Asp Asp Val Cys Pro Thr Glu Phe
                500                 505                 510

Glu Phe Val Thr Thr Glu Ala Pro Ala Val Asp Pro Asp Arg Arg
                515                 520                 525

Glu Val Asp Ser Ser Ala Ala Gln Arg Gly His Ser Leu Leu Ser
                530                 535                 540

Trp Ser Leu Thr Cys Ile Val Leu Ala Leu Gln Arg Leu Cys Arg
                545                 550                 555
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<210> 110
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 110
aagcgtgaca gcgggcacgt c 21

<210> 111
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 111

tgcacagtct ctgcagtgcc cagg 24

<210> 112
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 112
gaatgctgga acgggcacag caaagccaga tacttgcctg 40

<210> 113
<211> 4649
<212> DNA
<213> Homo sapiens

<400> 113
cggacgcgtg ggcggacgcg tgggcaaaag aactcggagt gccaaagcta 50

aataagttag ctgagaaaac gcacgcagtt tgcagcgcct gcgccgggtg 100

cgccaactac gcaaagacca agcgggctcc gcgcggaccg gccgcggggc 150

tagggacccg gctttggcct tcaggctccc tagcagcggg gaaaaggaat 200

tgctgcccgg agtttctgcg gaggtggagg gagatcagga aacggcttct 250

tcctcacttc gccgcctggt gagtgtcggg gagattggca aacgcctagg 300

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accccacaaa gcctatattt ttatatactg cctatcaagc tgttcattca 1700

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gggctgtagg ctttgtgcat agcccacttc tgaaaaacaa gggaacagtg 2000

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aacattgacc cctatacacc aaggcaaaaa atggctcctg ggcagcaggc 2200

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gaaattgctt acaggaaatc ctggctacag cgactgggtc ccccctcagt 2300

ctttcagcaa cctgggaccg aaccggtggc acaatgaacg gatcaccttg 2350

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cacatgtgaa cagcttgcac ctcattttac catgcgtgag ggaatggcaa 3200
ataagaatgt ttgagcacac tgcccacaat gaatgtaact attttctaaa 3250
cactttacta gaagaacatt tcagtataaa aaacctaatt tatttttaca 3300
gaaaaatatt ttgttgtttt tataaaaagt tatgcaaatg acttttattt 3350
ttatttcctg cataccatta gaagaatttt atttcatttc ttcaaattat 3400
caagcactgt aatactataa attaatgtaa tactgtgtga attcagacta 3450
taaaaaacat cattcagaaa actttataat cgtcattgtt caatcaagat 3500
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tgtggctttt ctgatctaac ttctagctaa aattgtatca ttggtcctaa 3700
aaaataaaaa tctttactaa taggcaattg aaggaatggt ttgctaacaa 3750
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acatggagaa agattttccc ataataataa ctaatattta tattaggttg 3850
gtgcaaaact agttgcggtt tttcccatta aaagtaataa ccttactctt 3900
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atacaaagtg gacactgtgg ggagatacag agaaatggaa gatacggatc 3950

ctgcctggag taggtaacct tgcttggaaa ccccacatgc aaacgtcatg 4000

aggagaatta aaggagtatt atcagtaatg aagtttatca tgggtcatca 4050

atgagcatag attggtgtgg atcctgtaga ccctggtgtt ttctttgaag 4100

tgccctctcc taatgcagag gccttgaagc ttacagtata cacttgaaaa 4150

gtcacagata gctagaatta tgatctttga agttataact gtgatctgaa 4200

aatgtgtgtg gtggtatgac agcataccat taaatacatt tacatcacag 4250

ctcaaaggac tgtgatataa tccatttata tcacaactca aaggactgtg 4300

atataatcca tttatatcac agctcacagt ttctgaaaat gtataaaaga 4350

atctataatc tagtactgaa attactaaat tgggtaagat gatttaaatg 4400

attttaattt taacatttta tttctagaat atatggctcc attttatttt 4450

atagtgtaaa gttgtatttc ctaaagtttg tgttttgtcg acagtatctt 4500

ttaaatgagt cttaaaaata aaggcatatt gttcatgttt aaaaaaaaaa 4550

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<210> 114
<211> 515
<212> PRT
<213> Homo sapiens

<400> 114
Met Ala Pro Arg Gly Cys Ala Gly His Pro Pro Pro Pro Ser Pro
1   5   10   15

Gln Ala Cys Val Cys Pro Gly Lys Met Leu Ala Met Gly Ala Leu
                20   25   30

Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly Tyr Leu Ser
                35   40   45

Trp Gly Gln Ala Leu Glu Glu Glu Glu Glu Gly Ala Leu Leu Ala
                50   55   60

Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln
                65   70   75

Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp
                80   85   90

Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys
                95   100   105

Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro

110 115 120

Ile Cys Thr Pro Ser Arg Ser Gln Phe Ile Thr Gly Lys Tyr Gln
125 130 135

Ile His Thr Gly Leu Gln His Ser Ile Ile Arg Pro Thr Gln Pro
140 145 150

Asn Cys Leu Pro Leu Asp Asn Ala Thr Leu Pro Gln Lys Leu Lys
155 160 165

Glu Val Gly Tyr Ser Thr His Met Val Gly Lys Trp His Leu Gly
170 175 180

Phe Asn Arg Lys Glu Cys Met Pro Thr Arg Arg Gly Phe Asp Thr
185 190 195

Phe Phe Gly Ser Leu Leu Gly Ser Gly Asp Tyr Tyr Thr His Tyr
200 205 210

Lys Cys Asp Ser Pro Gly Met Cys Gly Tyr Asp Leu Tyr Glu Asn
215 220 225

Asp Asn Ala Ala Trp Asp Tyr Asp Asn Gly Ile Tyr Ser Thr Gln
230 235 240

Met Tyr Thr Gln Arg Val Gln Gln Ile Leu Ala Ser His Asn Pro
245 250 255

Thr Lys Pro Ile Phe Leu Tyr Thr Ala Tyr Gln Ala Val His Ser
260 265 270

Pro Leu Gln Ala Pro Gly Arg Tyr Phe Glu His Tyr Arg Ser Ile
275 280 285

Ile Asn Ile Asn Arg Arg Arg Tyr Ala Ala Met Leu Ser Cys Leu
290 295 300

Asp Glu Ala Ile Asn Asn Val Thr Leu Ala Leu Lys Thr Tyr Gly
305 310 315

Phe Tyr Asn Asn Ser Ile Ile Ile Tyr Ser Ser Asp Asn Gly Gly
320 325 330

Gln Pro Thr Ala Gly Gly Ser Asn Trp Pro Leu Arg Gly Ser Lys
335 340 345

Gly Thr Tyr Trp Glu Gly Gly Ile Arg Ala Val Gly Phe Val His
350 355 360

Ser Pro Leu Leu Lys Asn Lys Gly Thr Val Cys Lys Glu Leu Val
365 370 375

His Ile Thr Asp Trp Tyr Pro Thr Leu Ile Ser Leu Ala Glu Gly
380 385 390

Gln Ile Asp Glu Asp Ile Gln Leu Asp Gly Tyr Asp Ile Trp Glu
395 400 405

Thr Ile Ser Glu Gly Leu Arg Ser Pro Arg Val Asp Ile Leu His
                410   415   420

Asn Ile Asp Pro Tyr Thr Pro Arg Gln Lys Met Ala Pro Gly Gln
                425   430   435

Gln Ala Met Gly Ser Gly Thr Leu Gln Ser Ser Gln Pro Ser Glu
                440   445   450

Cys Ser Thr Gly Asn Cys Leu Gln Glu Ile Leu Ala Thr Ala Thr
                455   460   465

Gly Ser Pro Leu Ser Leu Ser Ala Thr Trp Asp Arg Thr Gly Gly
                470   475   480

Thr Met Asn Gly Ser Pro Cys Gln Leu Ala Lys Val Tyr Gly Phe
                485   490   495

Ser Thr Ser Gln Pro Thr His Met Arg Gly Trp Thr Tyr Leu Thr
                500   505   510

Gly Ile Gln Glu Ser
                515

<210> 115
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 115
cccaacccaa ctgtttacct ctgg 24

<210> 116
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 116
ctctctgagt gtacatctgt gtgg 24

<210> 117
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<220>
<221> unsure
<222> 33
<223> unknown base

<400> 117
gccaccctac ctcagaaact gaaggaggtt ggntattcaa cgcatatggt 50

cgg 53

<210> 118
<211> 2260
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086
<223> unknown base

<400> 118
cggacgcgtg ggtgcgagtg gagcggagga cccgagcggc tgaggagaga 50

ggaggcggcg gcttagctgc tacggggtcc ggccggcgcc ctcccgaggg 100

gggctcagga ggaggaagga ggacccgtgc gagaatgcct ctgccctgga 150

gccttgcgct cccgctgctg ctctcctggg tggcaggtgg tttcgggaac 200

gcggccagtg caaggcatca cgggttgtta gcatcggcac gtcagcctgg 250

ggtctgtcac tatggaacta aactggcctg ctgctacggc tggagaagaa 300

acagcaaggg agtctgtgaa gctacatgcg aacctggatg taagtttggt 350

gagtgcgtgg gaccaaacaa atgcagatgc tttccaggat acaccgggaa 400

aacctgcagt caagatgtga atgagtgtgg aatgaaaccc cggccatgcc 450

aacacagatg tgtgaataca cacggaagct acaagtgctt ttgcctcagt 500

ggccacatgc tcatgccaga tgctacgtgt gtgaactcta ggacatgtgc 550

catgataaac tgtcagtaca gctgtgaaga cacagaagaa gggccacagt 600

gcctgtgtcc atcctcagga ctccgcctgg ccccaaatgg aagagactgt 650

ctagatattg atgaatgtgc ctctggtaaa gtcatctgtc cctacaatcg 700

aagatgtgtg aacacatttg gaagctacta ctgcaaatgt cacattggtt 750

tcgaactgca atatatcagt ggacgatatg actgtataga tataaatgaa 800

tgtactatgg atagccatac gtgcagccac catgccaatt gcttcaatac 850

ccaagggtcc ttcaagtgta aatgcaagca gggatataaa ggcaatggac 900

ttcggtgttc tgctatccct gaaaattctg tgaaggaagt cctcagagca 950

cctggtacca tcaaagacag aatcaagaag ttgcttgctc acaaaaacag 1000

catgaaaaag aaggcaaaaa ttaaaaatgt taccccagaa cccaccagga 1050 ctcctacccc taaggtgaac ttgcagccct tcaactatga agagatagtt 1100

tccagaggcg ggaactctca tggaggtaaa aaagggaatg aagagaaatg 1150

aaagaggggc ttgaggatga gaaaagagaa gagaaagccc tgaagaatga 1200

catagaggag cgaagcctgc gaggagatgt gtttttccct aaggtgaatg 1250

aagcaggtga attcggcctg attctggtcc aaaggaaagc gctaacttcc 1300

aaactggaac ataaagattt aaatatctcg gttgactgca gcttcaatca 1350

tgggatctgt gactggaaac aggatagaga agatgatttt gactggaatc 1400

ctgctgatcg agataatgct attggcttct atatggcagt tccggccttg 1450

gcaggtcaca agaaagacat tggccgattg aaacttctcc tacctgacct 1500

gcaaccccaa agcaacttct gtttgctctt tgattaccgg ctggccggag 1550

acaaagtcgg gaaacttcga gtgtttgtga aaaacagtaa caatgccctg 1600

gcatgggaga agaccacgag tgaggatgaa aagtggaaga cagggaaaat 1650

tcagttgtat caaggaactg atgctaccaa aagcatcatt tttgaagcag 1700

aacgtggcaa gggcaaaacc ggcgaaatcg cagtggatgg cgtcttgctt 1750

gtttcaggct tatgtccaga tagcctttta tctgtggatg actgaatgtt 1800

actatcttta tatttgactt tgtatgtcag ttccctggtt tttttgatat 1850

tgcatcatag gacctctggc attttagaat tactagctga aaaattgtaa 1900

tgtaccaaca gaaatattat tgtaagatgc ctttcttgta taagatatgc 1950

caatatttgc tttaaatatc atatcactgt atcttctcag tcatttctga 2000

atctttccnc attatattat aaaatntgga aangtcagtt tatctcccct 2050

cctcngtata tctgatttgt atangtangt tgatgngctt ctctctacaa 2100

catttctaga aaatagaaaa aaaagcacag agaaatgttt aactgtttga 2150

ctcttatgat acttcttgga aactatgaca tcaaagatag acttttgcct 2200

aagtggctta gctgggtctt tcatagccaa acttgtatat ttaattcttt 2250

gtaataataa 2260

<210> 119
<211> 338
<212> PRT
<213> Homo sapiens

<400> 119
Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu Ser Trp
1   5   10   15

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Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg His His Gly
                 20                  25                  30

Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr
                 35                  40                  45

Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val
                 50                  55                  60

Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val
                 65                  70                  75

Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr
                 80                  85                  90

Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys
                 95                 100                 105

Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys
                110                 115                 120

Leu Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser
                125                 130                 135

Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr
                140                 145                 150

Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu
                155                 160                 165

Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser
                170                 175                 180

Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe
                185                 190                 195

Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr
                200                 205                 210

Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met
                215                 220                 225

Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln
                230                 235                 240

Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly
                245                 250                 255

Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu
                260                 265                 270

Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala
                275                 280                 285

His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr
                290                 295                 300

Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro
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305 310 315

Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly
320 325 330

Gly Lys Lys Gly Asn Glu Glu Lys
335

<210> 120
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 120
cctcagtggc cacatgctca tg 22

<210> 121
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 121
ggctgcacgt atggctatcc atag 24

<210> 122
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 122
gataaactgt cagtacagct gtgaagacac agaagaaggg ccacagtgcc 50

<210> 123
<211> 1199
<212> DNA
<213> Homo sapiens

<400> 123
gggagctgct gctgtggctg ctggtgctgt gcgcgctgct cctgctcttg 50

gtgcagctgc tgcgcttcct gagggctgac ggcgacctga cgctactatg 100

ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatggtgg 150

tgtgggtgac tggagcctcg agtggaattg gtgaggagct ggcttaccag 200

ttgtctaaac taggagtttc tcttgtgctg tcagccagaa gagtgcatga 250

gctggaaagg gtgaaaagaa gatgcctaga gaatggcaat ttaaaagaaa 300

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aagatatact tgttttgccc cttgacctga ccgacactgg ttcccatgaa 350

gcggctacca aagctgttct ccaggagttt ggtagaatcg acattctggt 400

caacaatggt ggaatgtccc agcgttctct gtgcatggat accagcttgg 450

atgtctacag aaagctaata gagcttaact acttagggac ggtgtccttg 500

acaaaatgtg ttctgcctca catgatcgag aggaagcaag gaaagattgt 550

tactgtgaat agcatcctgg gtatcatatc tgtacctctt tccattggat 600

actgtgctag caagcatgct ctccggggtt tttttaatgg ccttcgaaca 650

gaacttgcca catacccagg tataatagtt tctaacattt gcccaggacc 700

tgtgcaatca aatattgtgg agaattccct agctggagaa gtcacaaaga 750

ctataggcaa taatggagac cagtcccaca agatgacaac cagtcgttgt 800

gtgcggctga tgttaatcag catggccaat gatttgaaag aagtttggat 850

ctcagaacaa cctttcttgt tagtaacata tttgtggcaa tacatgccaa 900

cctgggcctg gtggataacc aacaagatgg ggaagaaaag gattgagaac 950

tttaagagtg gtgtggatgc agactcttct tattttaaaa tctttaagac 1000

aaaacatgac tgaaaagagc acctgtactt ttcaagccac tggagggaga 1050

aatggaaaac atgaaaacag caatcttctt atgcttctga ataatcaaag 1100

actaatttgt gattttactt tttaatagat atgactttgc ttccaacatg 1150

gaatgaaata aaaaataaat aataaaagat tgccatgaat cttgcaaaa 1199
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<210> 124
<211> 289
<212> PRT
<213> Homo sapiens

<400> 124

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Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu
  1               5                  10                  15

Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
                 20                  25                  30

Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu
                 35                  40                  45

Glu Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu
                 50                  55                  60

Asp Leu Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val
                 65                  70                  75

Leu Gln Glu Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly
```

```
                80                  85                  90

Met Ser Gln Arg Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr
                95                  100                 105

Arg Lys Leu Ile Glu Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr
                110                 115                 120

Lys Cys Val Leu Pro His Met Ile Glu Arg Lys Gln Gly Lys Ile
                125                 130                 135

Val Thr Val Asn Ser Ile Leu Gly Ile Ile Ser Val Pro Leu Ser
                140                 145                 150

Ile Gly Tyr Cys Ala Ser Lys His Ala Leu Arg Gly Phe Phe Asn
                155                 160                 165

Gly Leu Arg Thr Glu Leu Ala Thr Tyr Pro Gly Ile Ile Val Ser
                170                 175                 180

Asn Ile Cys Pro Gly Pro Val Gln Ser Asn Ile Val Glu Asn Ser
                185                 190                 195

Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn Asn Gly Asp Gln
                200                 205                 210

Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu Met Leu Ile
                215                 220                 225

Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu Gln Pro
                230                 235                 240

Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp Ala
                245                 250                 255

Trp Trp Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe
                260                 265                 270

Lys Ser Gly Val Asp Ala Asp Ser Ser Tyr Phe Lys Ile Phe Lys
                275                 280                 285

Thr Lys His Asp
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<210> 125
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 125
gcaatgaact gggagctgc 19

<210> 126
<211> 19
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 126
ctgtgaatag catcctggg 19

<210> 127
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 127
cttttcaagc cactggaggg 20

<210> 128
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 128
ctgtagacat ccaagctggt atcc 24

<210> 129
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 129
aagagtctgc atccacacca ctc 23

<210> 130
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 130
acctgacgct actatgggcc gagtggcagg gacgacgccc agaatg 46

<210> 131
<211> 2365
<212> DNA
<213> Homo sapiens

<400> 131

gcgacgtggg caccgccatc agctgttcgc gcgtcttctc ctccaggtgg 50

ggcaggggtt tcgggctggt ggagcatgtg ctgggacagg acagcatcct 100

caatcaatcc aacagcatat tcggttgcat cttctacaca ctacagctat 150

tgttaggttg cctgcggaca cgctgggcct ctgtcctgat gctgctgagc 200

tccctggtgt ctctcgctgg ttctgtctac ctggcctgga tcctgttctt 250

cgtgctctat gatttctgca ttgtttgtat caccacctat gctatcaacg 300

tgagcctgat gtggctcagt ttccggaagg tccaagaacc ccagggcaag 350

gctaagaggc actgagccct caacccaagc caggctgacc tcatctgctt 400

tgctttggtc ttcaagccgc tcagcgtgcc tgtggacagc gtggccccgg 450

cccccccaag cctcaggagg gcaacacagt ccctggcgag tggccctggc 500

aggccagtgt gaggaggcaa ggagcccaca tctgcagcgg ctccctggtg 550

gcagacacct gggtcctcac tgctgcccac tgctttgaaa aggcagcagc 600

aacagaactg aattcctggt cagtggtcct gggttctctg cagcgtgagg 650

gactcagccc tggggccgaa gaggtggggg tggctgccct gcagttgccc 700

agggcctata accactacag ccagggctca gacctggccc tgctgcagct 750

cgcccacccc acgacccaca cacccctctg cctgccccag cccgcccatc 800

gcttcccctt tggagcctcc tgctgggcca ctggctggga tcaggacacc 850

agtgatgctc ctgggaccct acgcaatctg cgcctgcgtc tcatcagtcg 900

ccccacatgt aactgtatct acaaccagct gcaccagcga cacctgtcca 950

acccggcccg gcctgggatg ctatgtgggg gcccccagcc tggggtgcag 1000

ggcccctgtc agggagattc cgggggccct gtgctgtgcc tcgagcctga 1050

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gaggactggg tcagcagttt ggactggcag gtctacttcg ccgaggaacc 1950

agagcccgag gctgagcctg gaagctgcct ggccaacata agccaaccaa 2000

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aggcaaatgg cattactgcc cctgtcctcc ccaccctgtc atgtgtgatt 2100

ccaggcacca gggcaggccc agaagcccag cagctgtggg aaggaacctg 2150

cctggggcca caggtgccca ctccccaccc tgcaggacag gggtgtctgt 2200

ggacactccc acacccaact ctgctaccaa gcaggcgtct cagctttcct 2250

cctcctttac tctttcagat acaatcacgc cagccacgtt gttttgaaaa 2300

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tgttacaaaa taaaa 2365

<210> 132
<211> 571
<212> PRT
<213> Homo sapiens

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<400> 132
 Met Leu Leu Ser Ser Leu Val Ser Leu Ala Gly Ser Val Tyr Leu
   1               5                  10                  15

 Ala Trp Ile Leu Phe Phe Val Leu Tyr Asp Phe Cys Ile Val Cys
                  20                  25                  30

 Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe
                  35                  40                  45

 Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn
                  50                  55                  60

 Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln
                  65                  70                  75
```

Gly Ala His Ile Cys Ser Gly Ser Leu Val Ala Asp Thr Trp Val
80 85 90

Leu Thr Ala Ala His Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu
95 100 105

Asn Ser Trp Ser Val Val Leu Gly Ser Leu Gln Arg Glu Gly Leu
110 115 120

Ser Pro Gly Ala Glu Glu Val Gly Val Ala Ala Leu Gln Leu Pro
125 130 135

Arg Ala Tyr Asn His Tyr Ser Gln Gly Ser Asp Leu Ala Leu Leu
140 145 150

Gln Leu Ala His Pro Thr Thr His Thr Pro Leu Cys Leu Pro Gln
155 160 165

Pro Ala His Arg Phe Pro Phe Gly Ala Ser Cys Trp Ala Thr Gly
170 175 180

Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly Thr Leu Arg Asn Leu
185 190 195

Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn Cys Ile Tyr Asn
200 205 210

Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg Pro Gly Met
215 220 225

Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys Gln Gly
230 235 240

Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His Trp
245 250 255

Val Gln Ala Gly Ile Ile Ser Phe Ala Ser Ser Cys Ala Gln Glu
260 265 270

Asp Ala Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp
275 280 285

Leu Gln Ala Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro
290 295 300

Glu Thr Pro Glu Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly
305 310 315

Ser Leu Arg Thr Ala Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp
320 325 330

Pro Trp Glu Ala Arg Leu Met His Gln Gly Gln Leu Ala. Cys Gly
335 340 345

Gly Ala Leu Val Ser Glu Glu Ala Val Leu Thr Ala Ala His Cys
350 355 360

Phe Ile Gly Arg Gln Ala Pro Glu Glu Trp Ser Val Gly Leu Gly

365 370 375

Thr Arg Pro Glu Glu Trp Gly Leu Lys Gln Leu Ile Leu His Gly
380 385 390

Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp Met Ala Leu Leu Leu
395 400 405

Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu Arg Pro Leu Cys
410 415 420

Leu Pro Tyr Pro Asp His His Leu Pro Asp Gly Glu Arg Gly Trp
425 430 435

Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser Leu Gln
440 445 450

Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg Leu
455 460 465

His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met
470 475 480

Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly Leu
485 490 495

Ser Gly Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu
500 505 510

Ala Gly Leu His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg
515 520 525

Pro Ala Val Phe Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser
530 535 540

Ser Leu Asp Trp Gln Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu
545 550 555

Ala Glu Pro Gly Ser Cys Leu Ala Asn Ile Ser Gln Pro Thr Ser
560 565 570

Cys

<210> 133
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 133
cctgtgctgt gcctcgagcc tgac 24

<210> 134
<211> 24
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 134
gtgggcagca gttagcaccg cctc 24

<210> 135
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 135
ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136
<211> 1998
<212> DNA
<213> Homo sapiens

<400> 136
cgggccgccc ccggccccca ttcgggccgg gcctcgctgc ggcggcgact 50

gagccaggct gggccgcgtc cctgagtccc agagtcggcg cggcgcggca 100

ggggcagcct tccaccacgg ggagcccagc tgtcagccgc ctcacaggaa 150

gatgctgcgt cggcggggca gccctggcat gggtgtgcat gtgggtgcag 200

ccctgggagc actgtggttc tgcctcacag gagccctgga ggtccaggtc 250

cctgaagacc cagtggtggc actggtgggc accgatgcca ccctgtgctg 300

ctccttctcc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350

ggcagctgac agataccaaa cagctggtgc acagctttgc tgagggccag 400

gaccagggca gcgcctatgc caaccgcacg gccctcttcc cggacctgct 450

ggcacagggc aacgcatccc tgaggctgca gcgcgtgcgt gtggcggacg 500

agggcagctt cacctgcttc gtgagcatcc gggatttcgg cagcgctgcc 550

gtcagcctgc aggtggccgc tccctactcg aagcccagca tgaccctgga 600

gcccaacaag gacctgcggc caggggacac ggtgaccatc acgtgctcca 650

gctaccaggg ctaccctgag gctgaggtgt tctggcagga tgggcagggt 700

gtgcccctga ctggcaacgt gaccacgtcg cagatggcca acgagcaggg 750

cttgtttgat gtgcacagcg tcctgcgggt ggtgctgggt gcgaatggca 800

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gaccatgagg accagggagc tgctacccct ccctacagct cctaccctct 1150

ggctgcaatg gggctgcact gtgagccctg cccccaacag atgcatcctg 1200

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ctgccttatt tcaccaaaga cacgatgcat agtcaccccg gccttgtttc 1550

tccaatggcc gtgatacact agtgatcatg ttcagccctg cttccacctg 1600

catagaatct tttcttctca gacagggaca gtgcggcctc aacatctcct 1650

ggagtctaga agctgtttcc tttcccctcc ttcctccctg ccccaagtga 1700

agacagggca gggccaggaa tgctttgggg acaccgaggg gactgccccc 1750

cacccccacc atggtgctat tctggggctg gggcagtctt ttcctggctt 1800

gcctctggcc agctcctggc ctctggtaga gtgagacttc agacgttctg 1850

atgccttccg gatgtcatct ctccctgccc caggaatgga agatgtgagg 1900

acttctaatt taaatgtggg actcggaggg attttgtaaa ctgggggtat 1950

atttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaa 1998

<210> 137
<211> 316
<212> PRT
<213> Homo sapiens

<220>
<221> unsure
<222> 233
<223> unknown amino acid

<400> 137
Met Leu Arg Arg Arg Gly Ser Pro Gly Met Gly Val His Val Gly

1 5 10 15

Ala Ala Leu Gly Ala Leu Trp Phe Cys Leu Thr Gly Ala Leu Glu
20 25 30

Val Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp
35 40 45

Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu
50 55 60

Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu
65 70 75

Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala
80 85 90

Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala
95 100 105

Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe
110 115 120

Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser
125 130 135

Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu
140 145 150

Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys
155 160 165

Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp
170 175 180

Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met
185 190 195

Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val
200 205 210

Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro
215 220 225

Val Leu Gln Gln Asp Ala His Xaa Ser Val Thr Ile Thr Gly Gln
230 235 240

Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu
245 250 255

Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys
260 265 270

Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala
275 280 285

Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu Gln
290 295 300

Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile
305 310 315

Ala

<210> 138
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 138
ctggcacagc tcaacctcat ctgg 24

<210> 139
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 139
gctgtctgtc tgtctcattg 20

<210> 140
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 140
ggacacagta tactgaccac 20

<210> 141
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 141
tgcgaaccag gcagctgtaa gtgc 24

<210> 142
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 142
tggaagaaga gggtggtgat gtgg 24

<210> 143
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 143
cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144
<211> 2336
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1620, 1673
<223> unknown base

<400> 144
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gaagggggag tcctgaactt gtctgaagcc cttgtccgta agccttgaac 100

tacgttctta aatctatgaa gtcgagggac ctttcgctgc ttttgtaggg 150

acttctttcc ttgcttcagc aacatgaggc tttcttgtg gaacgcggtc 200

ttgactctgt tcgtcacttc tttgattggg gctttgatcc ctgaaccaga 250

agtgaaaatt gaagttctcc agaagccatt catctgccat cgcaagacca 300

aaggagggga tttgatgttg gtccactatg aaggctactt agaaaaggac 350

ggctccttat ttcactccac tcacaaacat aacaatggtc agcccatttg 400

gtttaccctg ggcatcctgg aggctctcaa aggttgggac cagggcttga 450

aaggaatgtg tgtaggagag aagagaaagc tcatcattcc tcctgctctg 500

ggctatggaa aagaaggaaa aggtaaaatt cccccagaaa gtacactgat 550

atttaatatt gatctcctgg agattcgaaa tggaccaaga tcccatgaat 600

cattccaaga aatggatctt aatgatgact ggaaactctc taaagatgag 650

gttaaagcat atttaaagaa ggagtttgaa aaacatggtg cggtggtgaa 700

tgaaagtcat catgatgctt tggtggagga tatttttgat aaagaagatg 750

aagacaaaga tgggtttata tctgccagag aatttacata taaacacgat 800

gagttataga gatacatcta cccttttaat atagcactca tctttcaaga 850

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gagggcagtc atctttaaag aacattttat ttttatacaa tgttctttct 900
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cccttaggtt tctaagtacc catttctttc tgataagtta ttgggaagaa 1000
aaagctaatt ggtctttgaa tagaagactt ctggacaatt tttcactttc 1050
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tcacttgaga tcaggagttc aagaccagcc tggccaacat ggtgaaacct 2100
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gcagctacta ttgaataaat acctatcctg gatttt 2336

<210> 145
<211> 211
<212> PRT
<213> Homo sapiens

<400> 145
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Met Arg Leu Phe Leu Trp Asn Ala Val Leu Thr Leu Phe Val Thr
  1               5                  10                  15

Ser Leu Ile Gly Ala Leu Ile Pro Glu Pro Glu Val Lys Ile Glu
                 20                  25                  30

Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly
                 35                  40                  45

Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly
                 50                  55                  60

Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile
                 65                  70                  75

Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln
                 80                  85                  90

Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile
                 95                 100                 105

Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro
                110                 115                 120

Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg
                125                 130                 135

Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn
                140                 145                 150

Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys
                155                 160                 165

Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His
                170                 175                 180

Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys
                185                 190                 195

Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu
                200                 205                 210

Leu
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<210> 146
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 146
ctttccttgc ttcagcaaca tgaggc 26

<210> 147
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 147
gcccagagca ggaggaatga tgagc 25

<210> 148
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 148
gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149
<211> 2196
<212> DNA
<213> Homo sapiens

<400> 149
aataaagctt ccttaatgtt gtatatgtct ttgaagtaca tccgtgcatt 50

tttttttagc atccaaccat tcctcccttg tagttctcgc cccctcaaat 100

caccctctcc cgtagcccac ccgactaaca tctcagtctc tgaaaatgca 150

cagagatgcc tggctacctc gccctgcctt cagcctcacg gggctcagtc 200

tctttttctc tttggtgcca ccaggacgga gcatggaggt cacagtacct 250

gccaccctca acgtcctcaa tggctctgac gcccgcctgc cctgcacctt 300

caactcctgc tacacagtga accacaaaca gttctccctg aactggactt 350

accaggagtg caacaactgc tctgaggaga tgttcctcca gttccgcatg 400

aagatcatta acctgaagct ggagcggttt caagaccgcg tggagttctc 450

agggaacccc agcaagtacg atgtgtcggt gatgctgaga aacgtgcagc 500

cggaggatga ggggatttac aactgctaca tcatgaaccc ccctgaccgc 550

caccgtggcc atggcaagat ccatctgcag gtcctcatgg aagagccccc 600

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tgcggccacg ctactcgctc ctctcccaac aactcccttc gtggggacaa 1900
aagtgacaat tgtaggccag gcacagtggc tcacgcctgt aatcccagca 1950
ctttgggagg ccaaggcggg tggattacct ccatctgttt agtagaaatg 2000
ggcaaaaccc catctctact aaaaatacaa gaattagctg ggcgtggtgg 2050
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cgtgtgcctg taatcccagc tatttgggag gctgaggcag gagaatcgct 2100

tgagcccggg aagcagaggt tgcagtgaac tgagatagtg atagtgccac 2150

tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150
<211> 215
<212> PRT
<213> Homo sapiens

<400> 150

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Met His Arg Asp Ala Trp Leu Pro Arg Pro Ala Phe Ser Leu Thr
 1               5                  10                  15

Gly Leu Ser Leu Phe Phe Ser Leu Val Pro Pro Gly Arg Ser Met
                20                  25                  30

Glu Val Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp
                35                  40                  45

Ala Arg Leu Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His
                50                  55                  60

Lys Gln Phe Ser Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys
                65                  70                  75

Ser Glu Glu Met Phe Leu Gln Phe Arg Met Lys Ile Ile Asn Leu
                80                  85                  90

Lys Leu Glu Arg Phe Gln Asp Arg Val Glu Phe Ser Gly Asn Pro
                95                 100                 105

Ser Lys Tyr Asp Val Ser Val Met Leu Arg Asn Val Gln Pro Glu
               110                 115                 120

Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg
               125                 130                 135

His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu
               140                 145                 150

Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser
               155                 160                 165

Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val
               170                 175                 180

Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp
               185                 190                 195

Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro
               200                 205                 210

Asp Asp Gly Ala Lys
               215
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<210> 151

<211> 524
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 103, 233
<223> unknown base

<400> 151
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tcctcccttg tagttctcgc cccctcaaat caccttctcc cttagcccac 100

ccnactaaca tctcagtctc tgaaaatgca cagagatgcc tggctacctc 150

gccctgcctt cagcctcacg gggctcagtc tctttttctc tttggtgcca 200

ccaggacgga gcatggaggt ccacagtacc tgnccaccct caacgtcctc 250

aatggctctg acgcccgcct gccctgccct tcaactcctg ctacacagtg 300

aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350

ctctgaggag atgttcctcc agttccgcat gaagatcatt aacctgaagc 400

tggagcggtt tcaagaccgc gtggagttct cagggaaccc cagcaagtac 450

gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500

caactgctac atcatgaacc cccc 524

<210> 152
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 56, 123
<223> unknown base

<400> 152
tcacggggct catctctttt tctctttggt gcccaccagg acggagcatg 50

gaggtncaca tacctgccac cctcaacgtc ctcaatggct ttgacgcccg 100

cctgccctgc accttcaact ccngctacac agtgaaccac aaacagttct 150

ccctgaactg gatttaccag gagtgcaaca actggctctg aggagatgtt 200

cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcggtt 250

ttcaagaacc gcgtggaagt ttctcaggga accccagcaa gtacgatgtg 300

tcggtgatgc tgagaaacgt gcagccggag gatgagggga tttacaactg 350

ctacatcatg aaccccccc 368

<210> 153
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 153
acggagcatg gaggtccaca gtac 24

<210> 154
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 154
gcacgtttct cagcatcacc gac 23

<210> 155
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155
cgcctgccct gcaccttcaa ctcctgctac acagtgaacc acaaacagtt 50

<210> 156
<211> 2680
<212> DNA
<213> Homo sapiens

<400> 156
tgcggcgacc gtcgtacacc atgggcctcc acctccgccc ctaccgtgtg 50

gggctgctcc cggatggcct cctgttcctc ttgctgctgc taatgctgct 100

cgcggaccca gcgctcccgg ccggacgtca ccccccagtg gtgctggtcc 150

ctggtgattt gggtaaccaa ctggaagcca agctggacaa gccgacagtg 200

gtgcactacc tctgctccaa gaagaccgaa agctacttca caatctggct 250

gaacctggaa ctgctgctgc ctgtcatcat tgactgctgg attgacaata 300

tcaggctggt ttacaacaaa acatccaggg ccacccagtt tcctgatggt 350

gtggatgtac gtgtccctgg ctttgggaag accttctcac tggagttcct 400

ggaccccagc aaaagcagcg tgggttccta tttccacacc atggtggaga 450

gccttgtggg ctggggctac acacggggtg aggatgtccg aggggctccc 500

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tatgactggc gccgagcccc aaatgaaaac gggccctact tcctggccct 550
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cccccagtcc cgcaggctgt gttccagggg ccctgatttc ctcggatgtg 2000

ctattggccc caggactgaa gctgcctccc ttcaccctgg gactgtggtt 2050

ccaaggatga gagcaggggt tggagccatg gccttctggg aacctatgga 2100

gaaagggaat ccaaggaagc agccaaggct gctcgcagct tccctgagct 2150

gcacctcttg ctaaccccac catcacactg ccaccctgcc ctagggtctc 2200

actagtacca agtgggtcag cacagggctg aggatggggc tcctatccac 2250

cctggccagc acccagctta gtgctgggac tagcccagaa acttgaatgg 2300

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<210> 157
<211> 412
<212> PRT
<213> Artificial

<400> 157

Met	Gly	Leu	His	Leu	Arg	Pro	Tyr	Arg	Val	Gly	Leu	Leu	Pro	Asp
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Gly	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Leu	Ala	Asp	Pro
				20					25					30
Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly
				35					40					45
Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val
				50					55					60
Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile
				65					70					75
Trp	Leu	Asn	Leu	Glu	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp
				80					85					90
Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr
				95					100					105
Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys

```
                    110                           115                           120

Thr Phe Ser Leu Glu Phe Leu Asp Pro Ser Lys Ser Ser Val Gly
                125                 130                 135

Ser Tyr Phe His Thr Met Val Glu Ser Leu Val Gly Trp Gly Tyr
                140                 145                 150

Thr Arg Gly Glu Asp Val Arg Gly Ala Pro Tyr Asp Trp Arg Arg
                155                 160                 165

Ala Pro Asn Glu Asn Gly Pro Tyr Phe Leu Ala Leu Arg Glu Met
                170                 175                 180

Ile Glu Glu Met Tyr Gln Leu Tyr Gly Gly Pro Val Val Leu Val
                185                 190                 195

Ala His Ser Met Gly Asn Met Tyr Thr Leu Tyr Phe Leu Gln Arg
                200                 205                 210

Gln Pro Gln Ala Trp Lys Asp Lys Tyr Ile Arg Ala Phe Val Ser
                215                 220                 225

Leu Gly Ala Pro Trp Gly Gly Val Ala Lys Thr Leu Arg Val Leu
                230                 235                 240

Ala Ser Gly Asp Asn Asn Arg Ile Pro Val Ile Gly Pro Leu Lys
                245                 250                 255

Ile Arg Glu Gln Gln Arg Ser Ala Val Ser Thr Ser Trp Leu Leu
                260                 265                 270

Pro Tyr Asn Tyr Thr Trp Ser Pro Glu Lys Val Phe Val Gln Thr
                275                 280                 285

Pro Thr Ile Asn Tyr Thr Leu Arg Asp Tyr Arg Lys Phe Phe Gln
                290                 295                 300

Asp Ile Gly Phe Glu Asp Gly Trp Leu Met Arg Gln Asp Thr Glu
                305                 310                 315

Gly Leu Val Glu Ala Thr Met Pro Pro Gly Val Gln Leu His Cys
                320                 325                 330

Leu Tyr Gly Thr Gly Val Pro Thr Pro Asp Ser Phe Tyr Tyr Glu
                335                 340                 345

Ser Phe Pro Asp Arg Asp Pro Lys Ile Cys Phe Gly Asp Gly Asp
                350                 355                 360

Gly Thr Val Asn Leu Lys Ser Ala Leu Gln Cys Gln Ala Trp Gln
                365                 370                 375

Ser Arg Gln Glu His Gln Val Leu Leu Gln Glu Leu Pro Gly Ser
                380                 385                 390

Glu His Ile Glu Met Leu Ala Asn Ala Thr Thr Leu Ala Tyr Leu
                395                 400                 405
```

Lys Arg Val Leu Leu Gly Pro
410

<210> 158
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 158
ctggggctac acacggggtg agg 23

<210> 159
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 159
ggtgccgctg cagaaagtag agcg 24

<210> 160
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 160
gccccaaatg aaaacgggcc ctacttcctg gccctccgcg agatg 45

<210> 161
<211> 1512
<212> DNA
<213> Homo sapiens

<400> 161
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gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150

tcttcgcctt gatcgtgttc tcctgcatct atggtgaggg ctacagcaat 200

gcccacgagt ctaagcagat gtactgcgtg ttcaaccgca acgaggatgc 250

ctgccgctat ggcagtgcca tcggggtgct ggccttcctg gcctcggcct 300

tcttcttggt ggtcgacgcg tatttccccc agatcagcaa cgccactgac 350

cgcaagtacc tggtcattgg tgacctgctc ttctcagctc tctggacctt 400 cctgtggttt gttggtttct gcttcctcac caaccagtgg gcagtcacca 450

acccgaagga cgtgctggtg ggggccgact ctgtgagggc agccatcacc 500

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gacaactacc aacagccacc cttcacccag aacgcggaga ccaccgaggg 700

ctaccagccg ccccctgtgt actgagtggc ggttagcgtg ggaaggggga 750

cagagagggc cctcccctct gccctggact ttcccatcag cctcctggaa 800

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gtgccccatg gctcccagac tctgtctgtg ccgagtgtat tataaaatcg 1450

tgggggagat gcccggcctg ggatgctgtt tggagacgga ataaatgttt 1500

tctcattcaa ag 1512

<210> 162
<211> 224
<212> PRT
<213> Homo sapiens

<400> 162
Met Glu Ser Gly Ala Tyr Gly Ala Ala Lys Ala Gly Gly Ser Phe
1 5 10 15

Asp Leu Arg Arg Phe Leu Thr Gln Pro Gln Val Val Ala Arg Ala
20 25 30

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Val Cys Leu Val Phe Ala Leu Ile Val Phe Ser Cys Ile Tyr Gly
                35                  40                  45

Glu Gly Tyr Ser Asn Ala His Glu Ser Lys Gln Met Tyr Cys Val
                50                  55                  60

Phe Asn Arg Asn Glu Asp Ala Cys Arg Tyr Gly Ser Ala Ile Gly
                65                  70                  75

Val Leu Ala Phe Leu Ala Ser Ala Phe Phe Leu Val Val Asp Ala
                80                  85                  90

Tyr Phe Pro Gln Ile Ser Asn Ala Thr Asp Arg Lys Tyr Leu Val
                95                  100                 105

Ile Gly Asp Leu Leu Phe Ser Ala Leu Trp Thr Phe Leu Trp Phe
                110                 115                 120

Val Gly Phe Cys Phe Leu Thr Asn Gln Trp Ala Val Thr Asn Pro
                125                 130                 135

Lys Asp Val Leu Val Gly Ala Asp Ser Val Arg Ala Ala Ile Thr
                140                 145                 150

Phe Ser Phe Phe Ser Ile Phe Ser Trp Gly Val Leu Ala Ser Leu
                155                 160                 165

Ala Tyr Gln Arg Tyr Lys Ala Gly Val Asp Asp Phe Ile Gln Asn
                170                 175                 180

Tyr Val Asp Pro Thr Pro Asp Pro Asn Thr Ala Tyr Ala Ser Tyr
                185                 190                 195

Pro Gly Ala Ser Val Asp Asn Tyr Gln Gln Pro Pro Phe Thr Gln
                200                 205                 210

Asn Ala Glu Thr Thr Glu Gly Tyr Gln Pro Pro Pro Val Tyr
                215                 220
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<210> 163
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 163
tggtcttcgc cttgatcgtg ttct 24

<210> 164
<211> 20
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 164
gtgtactgag cggcggttag 20

<210> 165
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 165
ctgaaggtga tggctgccct cac 23

<210> 166
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 166
ccaggaggct catgggaaag tcc 23

<210> 167
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 167
ccacgagtct aagcagatgt actgcgtgtt caaccgcaac gaggatgcct 50

<210> 168
<211> 3143
<212> DNA
<213> Homo sapiens

<400> 168
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agggtgatca gtgagcagaa ggatgcccgt ggccgaggcc ccccaggtgg 100

ctggcgggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150

atgttcaagg cctgtgagga ctccaagaga aaagcccggg gctacctccg 200

cctggtgccc ctgtttgtgc tgctggccct gctcgtgctg gcttcggcgg 250

gggtgctact ctggtatttc ctagggtaca aggcggaggt gatggtcagc 300

caggtgtact caggcagtct gcgtgtactc aatcgccact tctcccagga 350

tcttacccgc cgggaatcta gtgccttccg cagtgaaacc gccaaagccc 400

agaagatgct caaggagctc atcaccagca cccgcctggg aacttactac 450
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cctgggccct cacagcccag accctcactg ggaggtgagc tcagctgccc 3100

tttggaataa agctgcctga tcaaaaaaaa aaaaaaaaaa aaa 3143

<210> 169
<211> 802
<212> PRT
<213> Homo sapiens

<400> 169

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Met Pro Val Ala Glu Ala Pro Gln Val Ala Gly Gly Gln Gly Asp
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Gly Gly Asp Gly Glu Glu Ala Glu Pro Glu Gly Met Phe Lys Ala
                20                  25                  30

Cys Glu Asp Ser Lys Arg Lys Ala Arg Gly Tyr Leu Arg Leu Val
                35                  40                  45

Pro Leu Phe Val Leu Leu Ala Leu Leu Val Leu Ala Ser Ala Gly
                50                  55                  60

Val Leu Leu Trp Tyr Phe Leu Gly Tyr Lys Ala Glu Val Met Val
                65                  70                  75

Ser Gln Val Tyr Ser Gly Ser Leu Arg Val Leu Asn Arg His Phe
                80                  85                  90

Ser Gln Asp Leu Thr Arg Arg Glu Ser Ser Ala Phe Arg Ser Glu
                95                 100                 105

Thr Ala Lys Ala Gln Lys Met Leu Lys Glu Leu Ile Thr Ser Thr
               110                 115                 120

Arg Leu Gly Thr Tyr Tyr Asn Ser Ser Ser Val Tyr Ser Phe Gly
               125                 130                 135

Glu Gly Pro Leu Thr Cys Phe Phe Trp Phe Ile Leu Gln Ile Pro
               140                 145                 150

Glu His Arg Arg Leu Met Leu Ser Pro Glu Val Val Gln Ala Leu
               155                 160                 165

Leu Val Glu Glu Leu Leu Ser Thr Val Asn Ser Ser Ala Ala Val
               170                 175                 180

Pro Tyr Arg Ala Glu Tyr Glu Val Asp Pro Glu Gly Leu Val Ile
               185                 190                 195

Leu Glu Ala Ser Val Lys Asp Ile Ala Ala Leu Asn Ser Thr Leu
               200                 205                 210

Gly Cys Tyr Arg Tyr Ser Tyr Val Gly Gln Gly Gln Val Leu Arg
               215                 220                 225

Leu Lys Gly Pro Asp His Leu Ala Ser Ser Cys Leu Trp His Leu
               230                 235                 240

Gln Gly Pro Lys Asp Leu Met Leu Lys Leu Arg Leu Glu Trp Thr
               245                 250                 255

Leu Ala Glu Cys Arg Asp Arg Leu Ala Met Tyr Asp Val Ala Gly
               260                 265                 270

Pro Leu Glu Lys Arg Leu Ile Thr Ser Val Tyr Gly Cys Ser Arg
               275                 280                 285

Gln Glu Pro Val Val Glu Val Leu Ala Ser Gly Ala Ile Met Ala
```

```
                290                 295                 300

Val Val Trp Lys Lys Gly Leu His Ser Tyr Tyr Asp Pro Phe Val
                305                 310                 315

Leu Ser Val Gln Pro Val Val Phe Gln Ala Cys Glu Val Asn Leu
                320                 325                 330

Thr Leu Asp Asn Arg Leu Asp Ser Gln Gly Val Leu Ser Thr Pro
                335                 340                 345

Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln Thr His Cys Ser Trp His
                350                 355                 360

Leu Thr Val Pro Ser Leu Asp Tyr Gly Leu Ala Leu Trp Phe Asp
                365                 370                 375

Ala Tyr Ala Leu Arg Arg Gln Lys Tyr Asp Leu Pro Cys Thr Gln
                380                 385                 390

Gly Gln Trp Thr Ile Gln Asn Arg Arg Leu Cys Gly Leu Arg Ile
                395                 400                 405

Leu Gln Pro Tyr Ala Glu Arg Ile Pro Val Val Ala Thr Ala Gly
                410                 415                 420

Ile Thr Ile Asn Phe Thr Ser Gln Ile Ser Leu Thr Gly Pro Gly
                425                 430                 435

Val Arg Val His Tyr Gly Leu Tyr Asn Gln Ser Asp Pro Cys Pro
                440                 445                 450

Gly Glu Phe Leu Cys Ser Val Asn Gly Leu Cys Val Pro Ala Cys
                455                 460                 465

Asp Gly Val Lys Asp Cys Pro Asn Gly Leu Asp Glu Arg Asn Cys
                470                 475                 480

Val Cys Arg Ala Thr Phe Gln Cys Lys Glu Asp Ser Thr Cys Ile
                485                 490                 495

Ser Leu Pro Lys Val Cys Asp Gly Gln Pro Asp Cys Leu Asn Gly
                500                 505                 510

Ser Asp Glu Glu Gln Cys Gln Glu Gly Val Pro Cys Gly Thr Phe
                515                 520                 525

Thr Phe Gln Cys Glu Asp Arg Ser Cys Val Lys Lys Pro Asn Pro
                530                 535                 540

Gln Cys Asp Gly Arg Pro Asp Cys Arg Asp Gly Ser Asp Glu Glu
                545                 550                 555

His Cys Asp Cys Gly Leu Gln Gly Pro Ser Ser Arg Ile Val Gly
                560                 565                 570

Gly Ala Val Ser Ser Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
                575                 580                 585
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Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala Asp
                590                 595                 600

Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met
                605                 610                 615

Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln
                620                 625                 630

Asn Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu
                635                 640                 645

Leu Leu His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val
                650                 655                 660

Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val
                665                 670                 675

Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly
                680                 685                 690

Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly
                695                 700                 705

Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro
                710                 715                 720

Gln Asp Leu Cys Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg
                725                 730                 735

Met Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln
                740                 745                 750

Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg
                755                 760                 765

Trp Phe Leu Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg
                770                 775                 780

Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser
                785                 790                 795

Trp Ile Gln Gln Val Val Thr
                800
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<210> 170
<211> 1327
<212> DNA
<213> Homo sapiens

<400> 170
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atcctgcagc cctacgccga gaggatcccc gtggtggcca cggccgggat 100

caccatcaac ttcacctccc agatctccct caccgggccc ggtgtgcggg 150

tgcactatgg cttgtacaac cagtcggacc cctgccctgg agagttcctc 200
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tgttctgtga atggactctg tgtccctgcc tgtgatgggg tcaaggactg 250

ccccaacggc ctggatgaga gaaactgcgt ttgcagagcc acattccagt 300

gcaaagagga cagcacatgc atctcactgc ccaaggtctg tgatgggcag 350

cctgattgtc tcaacggcag cgatgaagag cagtgccagg aaggggtgcc 400

atgtgggaca ttcaccttcc agtgtgagga ccggagctgc gtgaagaagc 450

ccaacccgca gtgtgatggg cggcccgact gcagggacgg ctcggatgag 500

gagcactgtg actgtggcct ccagggcccc tccagccgca ttgttggtgg 550

agctgtgtcc tccgagggtg agtggccatg gcaggccagc ctccaggttc 600

ggggtcgaca catctgtggg ggggccctca tcgctgaccg ctgggtgata 650

acagctgccc actgcttcca ggaggacagc atggcctcca cggtgctgtg 700

gaccgtgttc ctgggcaagg tgtggcagaa ctcgcgctgg cctggagagg 750

tgtccttcaa ggtgagccgc ctgctcctgc acccgtacca cgaagaggac 800

agccatgact acgacgtggc gctgctgcag ctcgaccacc cggtggtgcg 850

ctcggccgcc gtgcgccccg tctgcctgcc cgcgcgctcc cacttcttcg 900

agcccggcct gcactgctgg attacgggct ggggcgcctt gcgcgagggc 950

ggccccatca gcaacgctct gcagaaagtg gatgtgcagt tgatcccaca 1000

ggacctgtgc agcgaggcct atcgctacca ggtgacgcca cgcatgctgt 1050

gtgccggcta ccgcaagggc aagaaggatg cctgtcaggg tgactcaggt 1100

ggtccgctgg tgtgcaaggc actcagtggc cgctggttcc tggcggggct 1150

ggtcagctgg ggcctgggct gtggccggcc taactacttc ggcgtctaca 1200

cccgcatcac aggtgtgatc agctggatcc agcaagtggt gacctgagga 1250

actgcccccc tgcaaagcag ggcccacctc ctggactcag agagcccagg 1300

gcaactgcca agcaggggga caagtat 1327

<210> 171
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 171
taacagctgc ccactgcttc cagg 24

<210> 172

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 172
taatccagca gtgcaggccg gg 22

<210> 173
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 173
atggcctcca cggtgctgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

<210> 174
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 174
tgcctatgca ctgaggaggc agaag 25

<210> 175
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 175
aggcagggac acagagtcca ttcac 25

<210> 176
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 176
agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

<210> 177
<211> 1510
<212> DNA
<213> Homo sapiens

<400> 177

ggacgagggc agatctcgtt ctggggcaag ccgttgacac tcgctccctg 50

ccaccgcccg ggctccgtgc cgccaagttt tcattttcca ccttctctgc 100

ctccagtccc ccagcccctg gccgagagaa gggtcttacc ggccgggatt 150

gctggaaaca ccaagaggtg gtttttgttt tttaaaactt ctgtttcttg 200

ggagggggtg tggcggggca ggatgagcaa ctccgttcct ctgctctgtt 250

tctggagcct ctgctattgc tttgctgcgg ggagccccgt accttttggt 300

ccagagggac ggctggaaga taagctccac aaacccaaag ctacacagac 350

tgaggtcaaa ccatctgtga ggtttaacct ccgcacctcc aaggacccag 400

agcatgaagg atgctacctc tccgtcggcc acagccagcc cttagaagac 450

tgcagtttca acatgacagc taaaaccttt ttcatcattc acggatggac 500

gatgagcggt atctttgaaa actggctgca caaactcgtg tcagccctgc 550

acacaagaga gaaagacgcc aatgtagttg tggttgactg gctccccctg 600

gcccaccagc tttacacgga tgcggtcaat aataccaggg tggtgggaca 650

cagcattgcc aggatgctcg actggctgca ggagaaggac gatttttctc 700

tcgggaatgt ccacttgatc ggctacagcc tcggagcgca cgtggccggg 750

tatgcaggca acttcgtgaa aggaacggtg ggccgaatca caggtttgga 800

tcctgccggg cccatgtttg aaggggccga catccacaag aggctctctc 850

cggacgatgc agattttgtg gatgtcctcc acacctacac gcgttccttc 900

ggcttgagca ttggtattca gatgcctgtg ggccacattg acatctaccc 950

caatgggggt gacttccagc caggctgtgg actcaacgat gtcttgggat 1000

caattgcata tggaacaatc acagaggtgg taaaatgtga gcatgagcga 1050

gccgtccacc tctttgttga ctctctggtg aatcaggaca agccgagttt 1100

tgccttccag tgcactgact ccaatcgctt caaaaagggg atctgtctga 1150

gctgccgcaa gaaccgttgt aatagcattg gctacaatgc caagaaaatg 1200

aggaacaaga ggaacagcaa aatgtaccta aaaacccggg caggcatgcc 1250

tttcagaggt aaccttcagt ccctggagtg tccctgagga aggcccttaa 1300

tacctccttc ttaataccat gctgcagagc agggcacatc ctagcccagg 1350

agaagtggcc agcacaatcc aatcaaatcg ttgcaaatca gattacactg 1400

tgcatgtcct aggaaaggga atctttacaa aataaacagt gtggacccct 1450

```
aataaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500

aaaaaaaaaa 1510

<210> 178
<211> 354
<212> PRT
<213> Homo sapiens

<400> 178
Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr
 1               5                  10                  15

Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg
                20                  25                  30

Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val
                35                  40                  45

Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu
                50                  55                  60

His Glu Gly Cys Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu
                65                  70                  75

Asp Cys Ser Phe Asn Met Thr Ala Lys Thr Phe Phe Ile Ile His
                80                  85                  90

Gly Trp Thr Met Ser Gly Ile Phe Glu Asn Trp Leu His Lys Leu
                95                 100                 105

Val Ser Ala Leu His Thr Arg Glu Lys Asp Ala Asn Val Val Val
               110                 115                 120

Val Asp Trp Leu Pro Leu Ala His Gln Leu Tyr Thr Asp Ala Val
               125                 130                 135

Asn Asn Thr Arg Val Val Gly His Ser Ile Ala Arg Met Leu Asp
               140                 145                 150

Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu Gly Asn Val His Leu
               155                 160                 165

Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly Tyr Ala Gly Asn
               170                 175                 180

Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu Asp Pro Ala
               185                 190                 195

Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu Ser Pro
               200                 205                 210

Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg Ser
               215                 220                 225

Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp
               230                 235                 240
```

```
Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn
                245                 250                 255

Asp Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val
                260                 265                 270

Lys Cys Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu
                275                 280                 285

Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser
                290                 295                 300

Asn Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg
                305                 310                 315

Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg
                320                 325                 330

Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg
                335                 340                 345

Gly Asn Leu Gln Ser Leu Glu Cys Pro
                350
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<210> 179
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 179
gtgagcatga gcgagccgtc cac 23

<210> 180
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 180
gctattacaa cggttcttgc ggcagc 26

<210> 181
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 181
ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240
<212> DNA
<213> Homo sapiens

<400> 182
cggacgcgtg ggcggacgcg tgggcctggg caagggccgg ggcgccgggc 50

cgagccacct cttcccctcc cccgcttccc tgtcgcgctc cgctggctgg 100

acgcgctgga ggagtggagc agcacccggc cggccctggg ggctgacagt 150

cggcaaagtt tggcccgaag aggaagtggt ctcaaacccc ggcaggtggc 200

gaccaggcca gaccaggggc gctcgctgcc tgcgggcggg ctgtaggcga 250

gggcgcgccc cagtgccgag acccggggct tcaggagccg gccccgggag 300

agaagagtgc ggcggcggac ggagaaaaca actccaaagt tggcgaaagg 350

caccgcccct actcccgggc tgccgccgcc tccccgcccc cagccctggc 400

atccagagta cgggtcgagc ccgggccatg gagcccccct ggggaggcgg 450

caccagggag cctgggcgcc cggggctccg ccgcgacccc atcgggtaga 500

ccacagaagc tccgggaccc ttccggcacc tctggacagc ccaggatgct 550

gttggccacc ctcctcctcc tcctccttgg aggcgctctg gcccatccag 600

accggattat ttttccaaat catgcttgtg aggacccccc agcagtgctc 650

ttagaagtgc agggcacctt acagaggccc ctggtccggg acagccgcac 700

ctcccctgcc aactgcacct ggctcatcct gggcagcaag gaacagactg 750

tcaccatcag gttccagaag ctacacctgg cctgtggctc agagcgctta 800

accctacgct cccctctcca gccactgatc tccctgtgtg aggcacctcc 850

cagccctctg cagctgcccg gggggcaacgt caccatcact tacagctatg 900

ctggggccag agcacccatg ggccagggct tcctgctctc ctacagccaa 950

gattggctga tgtgcctgca ggaagagttt cagtgcctga accaccgctg 1000

tgtatctgct gtccagcgct gtgatggggt tgatgcctgt ggcgatggct 1050

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ttcacagccc tggacttggg ctttggagat gcagtgcatg tgtatgacgg 1300

ccctgggccc cctgagagct cccgactact gcgtagtctc acccacttca 1350 gcaatggcaa ggctgtcact gtggagacac tgtctggcca ggctgttgtg 1400

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cagcgctgtg acggctcatg ggactgtgct gacggcacag atgaggagga 1600

ctgcccaggc tgcccacctg gacacttccc ctgtggggct gctggcacct 1650

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caatttccga tgccgggacg agaagtgcgt gtatgagacg tgggtgtgcg 1800

atgggcagcc agactgtgcg gacggcagtg atgagtggga ctgctcctat 1850

gttctgcccc gcaaggtcat tacagctgca gtcattggca gcctagtgtg 1900

cggcctgctc ctggtcatcg ccctgggctg cacctgcaag ctctatgcca 1950

ttcgcaccca ggagtacagc atctttgccc ccctctcccg gatggaggct 2000

gagattgtgc agcagcaggc acccccttcc tacgggcagc tcattgccca 2050

gggtgccatc ccacctgtag aagactttcc tacagagaat cctaatgata 2100

actcagtgct gggcaacctg cgttctctgc tacagatctt acgccaggat 2150

atgactccag gaggtggccc aggtgcccgc cgtcgtcagc ggggccgctt 2200

gatgcgacgc ctggtacgcc gtctccgccg ctggggcttg ctccctcgaa 2250

ccaacacccc ggctcgggcc tctgaggcca gatcccaggt cacaccttct 2300

gctgctcccc ttgaggccct agatggtggc acaggtccag cccgtgaggg 2350

cggggcagtg ggtgggcaag atggggagca ggcacccccca ctgcccatca 2400

aggctcccct cccatctgct agcacgtctc cagcccccac tactgtccct 2450

gaagccccag ggccactgcc ctcactgccc ctagagccat cactattgtc 2500

tggagtggtg caggccctgc gaggccgcct gttgcccagc ctggggcccc 2550

caggaccaac ccggagcccc cctggacccc acacagcagt cctggccctg 2600

gaagatgagg acgatgtgct actggtgcca ctggctgagc cgggggtgtg 2650

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ccaccatttg ggtggctgtt tttaaaaagt aaagttctta gaggatcata 3000

ggtctggaca ctccatcctt gccaaacctc tacccaaaag tggccttaag 3050

caccggaatg ccaattaact agagaccctc cagcccccaa ggggaggatt 3100

tgggcagaac ctgaggtttt gccatccaca atccctccta cagggcctgg 3150

ctcacaaaaa gagtgcaaca aatgcttcta ttccatagct acggcattgc 3200

tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183
<211> 713
<212> PRT
<213> Homo sapiens

<400> 183
Met Leu Leu Ala Thr Leu Leu Leu Leu Leu Leu Gly Gly Ala Leu
1 5 10 15

Ala His Pro Asp Arg Ile Ile Phe Pro Asn His Ala Cys Glu Asp
20 25 30

Pro Pro Ala Val Leu Leu Glu Val Gln Gly Thr Leu Gln Arg Pro
35 40 45

Leu Val Arg Asp Ser Arg Thr Ser Pro Ala Asn Cys Thr Trp Leu
50 55 60

Ile Leu Gly Ser Lys Glu Gln Thr Val Thr Ile Arg Phe Gln Lys
65 70 75

Leu His Leu Ala Cys Gly Ser Glu Arg Leu Thr Leu Arg Ser Pro
80 85 90

Leu Gln Pro Leu Ile Ser Leu Cys Glu Ala Pro Pro Ser Pro Leu
95 100 105

Gln Leu Pro Gly Gly Asn Val Thr Ile Thr Tyr Ser Tyr Ala Gly
110 115 120

Ala Arg Ala Pro Met Gly Gln Gly Phe Leu Leu Ser Tyr Ser Gln
125 130 135

Asp Trp Leu Met Cys Leu Gln Glu Glu Phe Gln Cys Leu Asn His
140 145 150

Arg Cys Val Ser Ala Val Gln Arg Cys Asp Gly Val Asp Ala Cys
155 160 165

Gly Asp Gly Ser Asp Glu Ala Gly Cys Ser Ser Asp Pro Phe Pro

170 175 180

Gly Leu Thr Pro Arg Pro Val Pro Ser Leu Pro Cys Asn Val Thr
185 190 195

Leu Glu Asp Phe Tyr Gly Val Phe Ser Ser Pro Gly Tyr Thr His
200 205 210

Leu Ala Ser Val Ser His Pro Gln Ser Cys His Trp Leu Leu Asp
215 220 225

Pro His Asp Gly Arg Arg Leu Ala Val Arg Phe Thr Ala Leu Asp
230 235 240

Leu Gly Phe Gly Asp Ala Val His Val Tyr Asp Gly Pro Gly Pro
245 250 255

Pro Glu Ser Ser Arg Leu Leu Arg Ser Leu Thr His Phe Ser Asn
260 265 270

Gly Lys Ala Val Thr Val Glu Thr Leu Ser Gly Gln Ala Val Val
275 280 285

Ser Tyr His Thr Val Ala Trp Ser Asn Gly Arg Gly Phe Asn Ala
290 295 300

Thr Tyr His Val Arg Gly Tyr Cys Leu Pro Trp Asp Arg Pro Cys
305 310 315

Gly Leu Gly Ser Gly Leu Gly Ala Gly Glu Gly Leu Gly Glu Arg
320 325 330

Cys Tyr Ser Glu Ala Gln Arg Cys Asp Gly Ser Trp Asp Cys Ala
335 340 345

Asp Gly Thr Asp Glu Glu Asp Cys Pro Gly Cys Pro Pro Gly His
350 355 360

Phe Pro Cys Gly Ala Ala Gly Thr Ser Gly Ala Thr Ala Cys Tyr
365 370 375

Leu Pro Ala Asp Arg Cys Asn Tyr Gln Thr Phe Cys Ala Asp Gly
380 385 390

Ala Asp Glu Arg Arg Cys Arg His Cys Gln Pro Gly Asn Phe Arg
395 400 405

Cys Arg Asp Glu Lys Cys Val Tyr Glu Thr Trp Val Cys Asp Gly
410 415 420

Gln Pro Asp Cys Ala Asp Gly Ser Asp Glu Trp Asp Cys Ser Tyr
425 430 435

Val Leu Pro Arg Lys Val Ile Thr Ala Ala Val Ile Gly Ser Leu
440 445 450

Val Cys Gly Leu Leu Leu Val Ile Ala Leu Gly Cys Thr Cys Lys
455 460 465

Leu Tyr Ala Ile Arg Thr Gln Glu Tyr Ser Ile Phe Ala Pro Leu
470 475 480

Ser Arg Met Glu Ala Glu Ile Val Gln Gln Gln Ala Pro Pro Ser
485 490 495

Tyr Gly Gln Leu Ile Ala Gln Gly Ala Ile Pro Pro Val Glu Asp
500 505 510

Phe Pro Thr Glu Asn Pro Asn Asp Asn Ser Val Leu Gly Asn Leu
515 520 525

Arg Ser Leu Leu Gln Ile Leu Arg Gln Asp Met Thr Pro Gly Gly
530 535 540

Gly Pro Gly Ala Arg Arg Arg Gln Arg Gly Arg Leu Met Arg Arg
545 550 555

Leu Val Arg Arg Leu Arg Arg Trp Gly Leu Leu Pro Arg Thr Asn
560 565 570

Thr Pro Ala Arg Ala Ser Glu Ala Arg Ser Gln Val Thr Pro Ser
575 580 585

Ala Ala Pro Leu Glu Ala Leu Asp Gly Gly Thr Gly Pro Ala Arg
590 595 600

Glu Gly Gly Ala Val Gly Gly Gln Asp Gly Glu Gln Ala Pro Pro
605 610 615

Leu Pro Ile Lys Ala Pro Leu Pro Ser Ala Ser Thr Ser Pro Ala
620 625 630

Pro Thr Thr Val Pro Glu Ala Pro Gly Pro Leu Pro Ser Leu Pro
635 640 645

Leu Glu Pro Ser Leu Leu Ser Gly Val Val Gln Ala Leu Arg Gly
650 655 660

Arg Leu Leu Pro Ser Leu Gly Pro Pro Gly Pro Thr Arg Ser Pro
665 670 675

Pro Gly Pro His Thr Ala Val Leu Ala Leu Glu Asp Glu Asp Asp
680 685 690

Val Leu Leu Val Pro Leu Ala Glu Pro Gly Val Trp Val Ala Glu
695 700 705

Ala Glu Asp Glu Pro Leu Leu Thr
710

<210> 184
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 184
ggctgtcact gtggagacac 20

<210> 185
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcaaggtcat tacagctg 18

<210> 186
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
agaacatagg agcagtccca ctc 23

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
tgcctgctgc tgcacaatct cag 23

<210> 188
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 188
ggctattgct tgccttggga cagaccctgt ggcttaggct ctggc 45

<210> 189
<211> 663
<212> DNA
<213> Homo sapiens

<400> 189
cgagctgggc gagaagtagg ggagggcggt gctccgccgc ggtggcggtt 50

gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150 aataaaacat cgccccttct gcttcagtgt gaaaggccac gtgaagatgc 200

tgcggctggc actaactgtg acatctatga cctttttat catcgcacaa 250

gcccctgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300

atttttcata cttttatatg tactcagact tgatcgatta atgaagtggt 350

tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400

atgctcatcg tatctgtgtt ggcactgata ccagaaacca caacattgac 450

agttggtgga ggggtgtttg cacttgtgac agcagtatgc tgtcttgccg 500

acggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550

cagaaaaagc ctgtgcatga aaaaaaagaa gttttgtaat tttatattac 600

tttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650

aaaaaaaaaa aaa 663

<210> 190
<211> 152
<212> PRT
<213> Homo sapiens

<400> 190

Met	Asp	Asn	Val	Gln	Pro	Lys	Ile	Lys	His	Arg	Pro	Phe	Cys	Phe
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Ser	Val	Lys	Gly	His	Val	Lys	Met	Leu	Arg	Leu	Ala	Leu	Thr	Val
				20					25					30
Thr	Ser	Met	Thr	Phe	Phe	Ile	Ile	Ala	Gln	Ala	Pro	Glu	Pro	Tyr
				35					40					45
Ile	Val	Ile	Thr	Gly	Phe	Glu	Val	Thr	Val	Ile	Leu	Phe	Phe	Ile
				50					55					60
Leu	Leu	Tyr	Val	Leu	Arg	Leu	Asp	Arg	Leu	Met	Lys	Trp	Leu	Phe
				65					70					75
Trp	Pro	Leu	Leu	Asp	Ile	Ile	Asn	Ser	Leu	Val	Thr	Thr	Val	Phe
				80					85					90
Met	Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro	Glu	Thr	Thr	Thr
				95					100					105
Leu	Thr	Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr	Ala	Val	Cys
				110					115					120
Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu	Phe	Asn
				125					130					135
Pro	Ser	Gly	Pro	Tyr	Gln	Lys	Lys	Pro	Val	His	Glu	Lys	Lys	Glu
				140					145					150

Val Leu

<210> 191
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 212, 234, 487
<223> unknown base

<400> 191
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ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100

ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150

catcgcccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200

ggcactaact gngacatcta tgaccttttt tatnatcgca caagcccctg 250

aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300

atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350

gcctttgctt gatattatca actcactggt aacaacagta ttcatgctca 400

tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggt 450

ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
cgttttgcag aacctactca ggcag 25

<210> 193
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 193
cctccaccaa ctgtcaatgt tgtgg 25

<210> 194
<211> 40

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 194
aaagtgctgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195
<211> 1879
<212> DNA
<213> Homo sapien

<400> 195
cagccccgcg cgccggccga gtcgctgagc cgcggctgcc ggacgggacg 50

ggaccggcta ggctgggcgc gcccccgggg ccccgccgtg ggcatgggcg 100

cactggcccg ggcgctgctg ctgcctctgc tggcccagtg gctcctgcgc 150

gccgccccgg agctggcccc cgcgcccttc acgctgcccc tccgggtggc 200

cgcggccacg aaccgcgtag ttgcgcccac cccgggaccc gggacccctg 250

ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc tgccctggcg 300

tcccccgcgg gcgccgccaa cttcttggcc atggtagaca acctgcaggg 350

ggactctggc cgcggctact acctggagat gctgatcggg acccccccgc 400

agaagctaca gattctcgtt gacactggaa gcagtaactt tgccgtggca 450

ggaaccccgc actcctacat agacacgtac tttgacacag agaggtctag 500

cacataccgc tccaagggct ttgacgtcac agtgaagtac acacaaggaa 550

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acacaagcaa acatccccaa cgttttctcc atgcagatgt gtggagccgg 800

cttgcccgtt gctggatctg ggaccaacgg aggtagtctt gtcttgggtg 850

gaattgaacc aagtttgtat aaaggagaca tctggtatac ccctattaag 900

gaagagtggt actaccagat agaaattctg aaattggaaa ttggaggcca 950

aagccttaat ctggactgca gagagtataa cgcagacaag gccatcgtgg 1000

acagtggcac cacgctgctg cgcctgcccc agaaggtgtt tgatgcggtg 1050

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aaataattaa aaaaaaaact tcattctaa 1879

<210> 196
<211> 518
<212> PRT
<213> Homo sapien

<400> 196

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Trp Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr
                20                  25                  30

Leu Pro Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro
                35                  40                  45

Thr Pro Gly Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu
                50                  55                  60

Ala Leu Ala Leu Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala
                65                  70                  75

Asn Phe Leu Ala Met Val Asp Asn Leu Gln Gly Asp Ser Gly Arg
                80                  85                  90

Gly Tyr Tyr Leu Glu Met Leu Ile Gly Thr Pro Pro Gln Lys Leu
                95                 100                 105
```

```
Gln Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Ala Gly
                110                 115                 120

Thr Pro His Ser Tyr Ile Asp Thr Tyr Phe Asp Thr Glu Arg Ser
                125                 130                 135

Ser Thr Tyr Arg Ser Lys Gly Phe Asp Val Thr Val Lys Tyr Thr
                140                 145                 150

Gln Gly Ser Trp Thr Gly Phe Val Gly Glu Asp Leu Val Thr Ile
                155                 160                 165

Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn Ile Ala Thr Ile
                170                 175                 180

Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys Trp Asn Gly
                185                 190                 195

Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser Ser Ser
                200                 205                 210

Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile Pro
                215                 220                 225

Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
                230                 235                 240

Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu
                245                 250                 255

Pro Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu
                260                 265                 270

Glu Trp Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly
                275                 280                 285

Gln Ser Leu Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala
                290                 295                 300

Ile Val Asp Ser Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val
                305                 310                 315

Phe Asp Ala Val Val Glu Ala Val Ala Arg Ala Ser Leu Ile Pro
                320                 325                 330

Glu Phe Ser Asp Gly Phe Trp Thr Gly Ser Gln Leu Ala Cys Trp
                335                 340                 345

Thr Asn Ser Glu Thr Pro Trp Ser Tyr Phe Pro Lys Ile Ser Ile
                350                 355                 360

Tyr Leu Arg Asp Glu Asn Ser Ser Arg Ser Phe Arg Ile Thr Ile
                365                 370                 375

Leu Pro Gln Leu Tyr Ile Gln Pro Met Met Gly Ala Gly Leu Asn
                380                 385                 390

Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro Ser Thr Asn Ala Leu
```

```
                    395                 400                 405

Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr Val Ile Phe Asp
                410                 415                 420

Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro Cys Ala Glu
                425                 430                 435

Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe Ser Thr
                440                 445                 450

Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser Glu
                455                 460                 465

Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
                470                 475                 480

Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg
                485                 490                 495

Cys Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser
                500                 505                 510

Ser Leu Val Arg His Arg Trp Lys
                515
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<210> 197
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 197
cgcagaagct acagattctc g 21

<210> 198
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 198
ggaaattgga ggccaaagc 19

<210> 199
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 199
ggatgtagcc agcaactgtg 20

<210> 200
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 200
gccttggctc gttctcttc 19

<210> 201
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 201
ggtcctgtgc ctggatgg 18

<210> 202
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 202
gacaagacta cctccgttgg tc 22

<210> 203
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 203
tgatgcacag ttcagcacct gttg 24

<210> 204
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 204
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205
<211> 1939
<212> DNA

<213> Homo sapiens

<400> 205
cgcctccgcc ttcggaggct gacgcgcccg ggcgccgttc caggcctgtg 50

cagggcggat cggcagccgc ctggcggcga tccagggcgg tgcggggcct 100

gggcgggagc cgggaggcgc ggccggcatg gaggcgctgc tgctgggcgc 150

ggggttgctg ctgggcgctt acgtgcttgt ctactacaac ctggtgaagg 200

ccccgccgtg cggcggcatg ggcaacctgc ggggccgcac ggccgtggtc 250

acgggcgcca acagcggcat cggaaagatg acggcgctgg agctggcgcg 300

ccggggagcg cgcgtggtgc tggcctgccg cagccaggag cgcggggagg 350

cggctgcctt cgacctccgc caggagagtg ggaacaatga ggtcatcttc 400

atggccttgg acttggccag tctggcctcg gtgcgggcct ttgccactgc 450

ctttctgagc tctgagccac ggttggacat cctcatccac aatgccggta 500

tcagttcctg tggccggacc cgtgaggcgt ttaacctgct gcttcgggtg 550

aaccatatcg gtccctttct gctgacacat ctgctgctgc cttgcctgaa 600

ggcatgtgcc cctagccgcg tggtggtggt agcctcagct gcccactgtc 650

ggggacgtct tgacttcaaa cgcctggacc gcccagtggt gggctggcgg 700

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cagggcaggg cagctggtat cgaggtgccc catgggagta aggggacgcc 1850

ttccgggcgg atgcagggct ggggtcatct gtatctgaag cccctcggaa 1900

taaagcgcgt tgaccgccaa aaaaaaaaaa aaaaaaaaa 1939

<210> 206
<211> 377
<212> PRT
<213> Homo sapiens

<400> 206

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Met Glu Ala Leu Leu Leu Gly Ala Gly Leu Leu Leu Gly Ala Tyr
 1               5                  10                  15

Val Leu Val Tyr Tyr Asn Leu Val Lys Ala Pro Pro Cys Gly Gly
            20                  25                  30

Met Gly Asn Leu Arg Gly Arg Thr Ala Val Val Thr Gly Ala Asn
            35                  40                  45

Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly
            50                  55                  60

Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala
            65                  70                  75

Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile
            80                  85                  90

Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe
            95                 100                 105

Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile
           110                 115                 120

His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe
           125                 130                 135

Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr
           140                 145                 150
```

```
His Leu Leu Leu Pro Cys Leu Lys Ala Cys Ala Pro Ser Arg Val
                155                 160                 165

Val Val Val Ala Ser Ala Ala His Cys Arg Gly Arg Leu Asp Phe
                170                 175                 180

Lys Arg Leu Asp Arg Pro Val Val Gly Trp Arg Gln Glu Leu Arg
                185                 190                 195

Ala Tyr Ala Asp Thr Lys Leu Ala Asn Val Leu Phe Ala Arg Glu
                200                 205                 210

Leu Ala Asn Gln Leu Glu Ala Thr Gly Val Thr Cys Tyr Ala Ala
                215                 220                 225

His Pro Gly Pro Val Asn Ser Glu Leu Phe Leu Arg His Val Pro
                230                 235                 240

Gly Trp Leu Arg Pro Leu Leu Arg Pro Leu Ala Trp Leu Val Leu
                245                 250                 255

Arg Ala Pro Arg Gly Gly Ala Gln Thr Pro Leu Tyr Cys Ala Leu
                260                 265                 270

Gln Glu Gly Ile Glu Pro Leu Ser Gly Arg Tyr Phe Ala Asn Cys
                275                 280                 285

His Val Glu Glu Val Pro Pro Ala Ala Arg Asp Asp Arg Ala Ala
                290                 295                 300

His Arg Leu Trp Glu Ala Ser Lys Arg Leu Ala Gly Leu Gly Pro
                305                 310                 315

Gly Glu Asp Ala Glu Pro Asp Glu Asp Pro Gln Ser Glu Asp Ser
                320                 325                 330

Glu Ala Pro Ser Ser Leu Ser Thr Pro His Pro Glu Glu Pro Thr
                335                 340                 345

Val Ser Gln Pro Tyr Pro Ser Pro Gln Ser Ser Pro Asp Leu Ser
                350                 355                 360

Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln
                365                 370                 375

Leu Ser
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<210> 207
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 207
cttcatggcc ttggacttgg ccag 24

<210> 208
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 208
acgccagtgg cctcaagctg gttg 24

<210> 209
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 209
ctttctgagc tctgagccac ggttggacat cctcatccac aatgc 45

<210> 210
<211> 3716
<212> DNA
<213> Homo sapiens

<400> 210
ggaggagaca gcctcctggg gggcaggggt tccctgcctc tgctgctcct 50

gctcatcatg ggaggcatgg ctcaggactc cccgccccag atcctagtcc 100

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caagcctcag gccagccacc tcccaccatc cgctggttgc tgaatgggca 200

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atggtggaaa gatgggaaac ccctggccct ccagcccgga aggcacacag 550

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tatgagaccg taggtcaaaa gcaccatcct cgtactgttg tcactatgag 3650 cttaagaaat ttgataccat aaaatggtaa aaaaaaaaaa aaaaaaaaaa 3700

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<210> 211
<211> 985
<212> PRT
<213> Homo sapiens

<400> 211
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Met Gly Gly Met Ala Gln Asp Ser Pro Pro Gln Ile Leu Val His
 1               5                  10                  15

Pro Gln Asp Gln Leu Phe Gln Gly Pro Gly Pro Ala Arg Met Ser
                20                  25                  30

Cys Gln Ala Ser Gly Gln Pro Pro Pro Thr Ile Arg Trp Leu Leu
                35                  40                  45

Asn Gly Gln Pro Leu Ser Met Val Pro Pro Asp Pro His His Leu
                50                  55                  60

Leu Pro Asp Gly Thr Leu Leu Leu Leu Gln Pro Pro Ala Arg Gly
                65                  70                  75

His Ala His Asp Gly Gln Ala Leu Ser Thr Asp Leu Gly Val Tyr
                80                  85                  90

Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr Ala Val Ser Arg Gly
                95                 100                 105

Ala Arg Leu Ser Val Ala Val Leu Arg Glu Asp Phe Gln Ile Gln
               110                 115                 120

Pro Arg Asp Met Val Ala Val Val Gly Glu Gln Phe Thr Leu Glu
               125                 130                 135

Cys Gly Pro Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp
               140                 145                 150

Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val
               155                 160                 165

Ser Gly Gly Ser Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu
               170                 175                 180

Gly Thr Tyr Met Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu
               185                 190                 195

Ser Arg Ala Ala Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr
               200                 205                 210

Glu Pro Val Glu Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val
               215                 220                 225

Thr Leu Leu Asn Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro
               230                 235                 240
```

```
Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala
                245                 250                 255

Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly
                260                 265                 270

Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser
                275                 280                 285

Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys
                290                 295                 300

Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val
                305                 310                 315

Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln
                320                 325                 330

Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp
                335                 340                 345

Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr
                350                 355                 360

Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp
                365                 370                 375

Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met
                380                 385                 390

Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly
                395                 400                 405

Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala
                410                 415                 420

Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr
                425                 430                 435

Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala
                440                 445                 450

Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Leu Gly Thr Ala Val
                455                 460                 465

Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly
                470                 475                 480

Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met
                485                 490                 495

Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr
                500                 505                 510

Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg
                515                 520                 525

Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu
```

```
                530                 535                 540

Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu Leu Pro Asp
                545                 550                 555

Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser
                560                 565                 570

Thr Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu
                575                 580                 585

Pro Pro Gln Leu Ala Gln Leu Ser Ser Pro Cys Ser Ser Ser Asp
                590                 595                 600

Ser Leu Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu
                605                 610                 615

Ala Pro Ala Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln
                620                 625                 630

His Ala Asn Ser Ser Pro Leu Leu Arg Gly Ser His Ser Leu Glu
                635                 640                 645

Leu Arg Ala Cys Glu Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser
                650                 655                 660

Gln Ser Pro Gly Ala Val Pro Gln Ala Leu Val Ala Trp Arg Ala
                665                 670                 675

Leu Gly Pro Lys Leu Leu Ser Ser Ser Asn Glu Leu Val Thr Arg
                680                 685                 690

His Leu Pro Pro Ala Pro Leu Phe Pro His Glu Thr Pro Pro Thr
                695                 700                 705

Gln Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser
                710                 715                 720

Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys
                725                 730                 735

Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro
                740                 745                 750

Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser Leu Gly Glu
                755                 760                 765

Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys Leu
                770                 775                 780

Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro
                785                 790                 795

Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser
                800                 805                 810

Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly
                815                 820                 825
```

```
Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro
                830                 835                 840

Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp
                845                 850                 855

Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu
                860                 865                 870

Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala
                875                 880                 885

Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu
                890                 895                 900

Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro
                905                 910                 915

Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro
                920                 925                 930

Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser
                935                 940                 945

His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp
                950                 955                 960

Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro
                965                 970                 975

Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser
                980                 985
```

```
<210> 212
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 212
 gaagggacct acatgtgtgt ggcc 24

<210> 213
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 213
 actgaccttc cagctgagcc acac 24

<210> 214
<211> 50
<212> DNA
```

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 214
aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215
<211> 2749
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1869, 1887
<223> unknown base

<400> 215
ctcccacggt gtccagcgcc cagaatgcgg cttctggtcc tgctatgggg 50

ttgcctgctg ctcccaggtt atgaagccct ggagggccca gaggaaatca 100

gcgggttcga aggggacact gtgtccctgc agtgcaccta cagggaagag 150

ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200

tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250

agggcagggt gtccatccgt gacagccgcc aggagctctc gctcattgtg 300

accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtggggt 350

cgaaaaacgg ggccccgatg agtctttact gatctctctg ttcgtctttc 400

caggaccctg ctgtcctccc tccccttctc ccaccttcca gcctctggct 450

acaacacgcc tgcagcccaa ggcaaaagct cagcaaaccc agcccccagg 500

attgacttct cctgggctct acccggcagc caccacagcc aagcagggga 550

agacaggggc tgaggcccct ccattgccag ggacttccca gtacgggcac 600

gaaaggactt ctcagtacac aggaacctct cctcacccag cgacctctcc 650

tcctgcaggg agctcccgcc cccccatgca gctggactcc acctcagcag 700

aggacaccag tccagctctc agcagtggca gctctaagcc cagggtgtcc 750

atcccgatgg tccgcatact ggccccagtc ctggtgctgc tgagccttct 800

gtcagccgca ggcctgatcg ccttctgcag ccacctgctc ctgtggagaa 850

aggaagctca acaggccacg gagacacaga ggaacgagaa gttctggctc 900

tcacgcttga ctgcggagga aaaggaagcc ccttcccagg cccctgaggg 950

ggacgtgatc tcgatgcctc cctccacac atctgaggag gagctgggct 1000 tctcgaagtt tgtctcagcg tagggcagga ggccctcctg gccaggccag 1050

cagtgaagca gtatggctgg ctggatcagc accgattccc gaaagctttc 1100

cacctcagcc tcagagtcca gctgcccgga ctccagggct ctccccaccc 1150

tccccaggct ctcctcttgc atgttccagc ctgacctaga agcgtttgtc 1200

agccctggag cccagagcgg tggccttgct cttccggctg gagactggga 1250

catccctgat aggttcacat ccctgggcag agtaccaggc tgctgaccct 1300

cagcagggcc agacaaggct cagtggatct ggtctgagtt tcaatctgcc 1350

aggaactcct gggcctcatg cccagtgtcg gaccctgcct tcctcccact 1400

ccagacccca ccttgtcttc cctccctggc gtcctcagac ttagtcccac 1450

ggtctcctgc atcagctggt gatgaagagg agcatgctgg ggtgagactg 1500

ggattctggc ttctctttga accacctgca tccagccctt caggaagcct 1550

gtgaaaaacg tgattcctgg ccccaccaag acccaccaaa accatctctg 1600

ggcttggtgc aggactctga attctaacaa tgcccagtga ctgtcgcact 1650

tgagtttgag ggccagtggg cctgatgaac gctcacaccc cttcagctta 1700

gagtctgcat ttgggctgtg acgtctccac ctgccccaat agatctgctc 1750

tgtctgcgac accagatcca cgtggggact cccctgaggc ctgctaagtc 1800

caggccttgg tcaggtcagg tgcacattgc aggataagcc caggaccggc 1850

acagaagtgg ttgcctttnc catttgccct ccctggncca tgccttcttg 1900

cctttggaaa aaatgatgaa gaaaaccttg gctccttcct tgtctggaaa 1950

gggttacttg cctatgggtt ctggtggcta gagagaaaag tagaaaacca 2000

gagtgcacgt aggtgtctaa cacagaggag agtaggaaca gggcggatac 2050

ctgaaggtga ctccgagtcc agccccctgg agaaggggtc gggggtggtg 2100

gtaaagtagc acaactacta tttttttct ttttccatta ttattgtttt 2150

ttaagacaga atctcgtgct gctgcccagg ctggagtgca gtggcacgat 2200

ctgcaaactc cgcctcctgg gttcaagtga ttcttctgcc tcagcctccc 2250

gagtagctgg gattacaggc acgcaccacc acacctggct aatttttgta 2300

cttttagtag agatggggtt tcaccatgtt ggccaggctg gtcttgaact 2350

cctgacctca aatgagcctc ctgcttcagt ctcccaaatt gccgggatta 2400

caggcatgag ccactgtgtc tggccctatt tcctttaaaa agtgaaatta 2450

```
agagttgttc agtatgcaaa acttggaaag atggaggaga aaaagaaaag 2500

gaagaaaaaa atgtcaccca tagtctcacc agagactatc attatttcgt 2550

tttgttgtac ttccttccac tcttttcttc ttcacataat ttgccggtgt 2600

tctttttaca gagcaattat cttgtatata caactttgta tcctgccttt 2650

tccaccttat cgttccatca ctttattcca gcacttctct gtgttttaca 2700

gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaa 2749
```

```
<210> 216
<211> 332
<212> PRT
<213> Homo sapiens

<400> 216
Met Arg Leu Leu Val Leu Leu Trp Gly Cys Leu Leu Leu Pro Gly
  1               5                  10                  15

Tyr Glu Ala Leu Glu Gly Pro Glu Glu Ile Ser Gly Phe Glu Gly
                 20                  25                  30

Asp Thr Val Ser Leu Gln Cys Thr Tyr Arg Glu Glu Leu Arg Asp
                 35                  40                  45

His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg
                 50                  55                  60

Cys Ser Gly Thr Ile Tyr Ala Glu Glu Glu Gly Gln Glu Thr Met
                 65                  70                  75

Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu
                 80                  85                  90

Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr
                 95                 100                 105

Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile
                110                 115                 120

Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser
                125                 130                 135

Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala
                140                 145                 150

Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu
                155                 160                 165

Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu
                170                 175                 180

Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr
                185                 190                 195

Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro
```

```
                200                 205                 210

Ala Gly Ser Ser Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala
                215                 220                 225

Glu Asp Thr Ser Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg
                230                 235                 240

Val Ser Ile Pro Met Val Arg Ile Leu Ala Pro Val Leu Val Leu
                245                 250                 255

Leu Ser Leu Leu Ser Ala Ala Gly Leu Ile Ala Phe Cys Ser His
                260                 265                 270

Leu Leu Leu Trp Arg Lys Glu Ala Gln Gln Ala Thr Glu Thr Gln
                275                 280                 285

Arg Asn Glu Lys Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys
                290                 295                 300

Glu Ala Pro Ser Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro
                305                 310                 315

Pro Leu His Thr Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val
                320                 325                 330

Ser Ala
```

```
<210> 217
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 217
 ccctgcagtg cacctacagg gaag 24

<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 218
 ctgtcttccc ctgcttggct gtgg 24

<210> 219
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe
```

<400> 219
ggtgcaggaa gggtgggatc ctcttctctc gctgctctgg ccacatc 47

<210> 220
<211> 950
<212> DNA
<213> Homo sapiens

<400> 220
ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50

ggggtggcag gagccgcaga gccagagcag acagccgaga aacaggtgga 100

cagtgtgaaa gaaccagtgg tctcgctctg ttgcccaggc tagagtgtac 150

tggcgtgatc atagctcact gcagcctcag actcctggac ttgagaaatc 200

ctcctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250

cctgtttctt ctccttctgt gagtggacca cggaggctgg tgagctgcct 300

gtcatcccaa agctcagctc tgagccagag tggtggtggc tccacctctg 350

ccgccggcat agaagccagg agcagggctc tcagaaggcg gtggtgccca 400

gctgggatca tgttgttggc cctggtctgt ctgctcagct gcctgctacc 450

ctccagtgag gccaagctct acggtcgttg tgaactggcc agagtgctac 500

atgacttcgg gctggacgga taccggggat acagcctggc tgactgggtc 550

tgccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600

ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650

ggtgcagcaa cctcaccccg aacgtcccca acgtgtgccg gatgtactgc 700

tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750

gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800

actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850

gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900

cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221
<211> 146
<212> PRT
<213> Homo sapiens

<400> 221
Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser
1 5 10 15

Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu
20 25 30

His Asp Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp
35 40 45

Trp Val Cys Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala
50 55 60

Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln
65 70 75

Ile Asn Ser Arg Arg Trp Cys Ser Asn Leu Thr Pro Asn Val Pro
80 85 90

Asn Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu
95 100 105

Lys Asp Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln
110 115 120

Gly Leu Gly Tyr Trp Glu Ala Trp Arg His His Cys Gln Gly Lys
125 130 135

Asp Leu Thr Glu Trp Val Asp Gly Cys Asp Phe
140 145

<210> 222
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 222
gggatcatgt tgttggccct ggtc 24

<210> 223
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 223
gcaaggcaga cccagtcagc cag 23

<210> 224
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 224
ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225

<211> 2049
<212> DNA
<213> Homo sapiens

<400> 225
agccgctgcc ccgggccggg cgcccgcggc ggcaccatga gtccccgctc 50

gtgcctgcgt tcgctgcgcc tcctcgtctt cgccgtcttc tcagccgccg 100

cgagcaactg gctgtacctg gccaagctgt cgtcggtggg gagcatctca 150

gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200

gatgtgcaag cggaacctgg aagtcatgga ctcggtgcgc cgcggtgccc 250

agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300

tgctccacac tcgactcctt gcccgtcttc ggcaaggtgg tgacgcaagg 350

gactcgggag gcggccttcg tgtacgccat ctcttcggca ggtgtggcct 400

ttgcagtgac gcgggcgtgc agcagtgggg agctggagaa gtgcggctgt 450

gacaggacag tgcatggggt cagcccacag ggcttccagt ggtcaggatg 500

ctctgacaac atcgcctacg gtgtggcctt ctcacagtcg tttgtggatg 550

tgcgggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600

cacaacaatg aggccggcag gaaggccatc ctgacacaca tgcgggtgga 650

atgcaagtgc cacggggtgt caggctcctg tgaggtaaag acgtgctggc 700

gagccgtgcc gcccttccgc caggtgggtc acgcactgaa ggagaagttt 750

gatggtgcca ctgaggtgga gccacgccgc gtgggctcct ccagggcact 800

ggtaccacgc aacgcacagt tcaagccgca cacagatgag gacctggtgt 850

acttggagcc tagccccgac ttctgtgagc aggacatgcg cagcggcgtg 900

ctgggcacga ggggccgcac atgcaacaag acgtccaagg ccatcgacgg 950

ctgtgagctg ctgtgctgtg gccgcggctt ccacacggcg caggtggagc 1000

tggctgaacg ctgcagctgc aaattccact ggtgctgctt cgtcaagtgc 1050

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ctagccctgc gccggcaacc acctagtggc ccagggaagg ccgataattt 1150

aaacagtctc ccaccaccta ccccaagaga tactggttgt atttttgtt 1200

ctggtttggt ttttgggtcc tcatgttatt tattgccgaa accaggcagg 1250

caaccccaag ggcaccaacc agggcctccc caaagcctgg gcctttgtgg 1300

ctgccactga ccaaagggac cttgctcgtg ccgctggctg cccgcatgtg 1350 gctgccactg accactcagt tgttatctgt gtccgttttt ctacttgcag 1400

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gtcatcgggg aagagggggc cttatggcag ggaaaatagg taccgacttg 1500

atggaagtca caccctctgg aaaaaagaac tcttaactct ccagcacaca 1550

tacacatgga ctcctggcag cttgagccta gaagccatgt ctctcaaatg 1600

ccctgagaaa gggaacaagc agataccagg tcaagggcac caggttcatt 1650

tcagccctta catggacagc tagaggttcg atatctgtgg gtccttccag 1700

gcaagaagag ggagatgaga gcaagagacg actgaagtcc caccctagaa 1750

cccagcctgc cccagcctgc ccctgggaag aggaaactta accactcccc 1800

agacccacct aggcaggcat ataggctgcc atcctggacc agggatcccg 1850

gctgtgcctt tgcagtcatg cccgagtcac ctttcacagc gctgttcctc 1900

catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950

acacacacac ggacacacac acacacctgc gagagagagg gaggaaaggg 2000

ctgtgccttt gcagtcatgc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226
<211> 351
<212> PRT
<213> Homo sapiens

<400> 226
Met Ser Pro Arg Ser Cys Leu Arg Ser Leu Arg Leu Leu Val Phe
1   5   10   15

Ala Val Phe Ser Ala Ala Ala Ser Asn Trp Leu Tyr Leu Ala Lys
            20   25   30

Leu Ser Ser Val Gly Ser Ile Ser Glu Glu Glu Thr Cys Glu Lys
            35   40   45

Leu Lys Gly Leu Ile Gln Arg Gln Val Gln Met Cys Lys Arg Asn
            50   55   60

Leu Glu Val Met Asp Ser Val Arg Arg Gly Ala Gln Leu Ala Ile
            65   70   75

Glu Glu Cys Gln Tyr Gln Phe Arg Asn Arg Arg Trp Asn Cys Ser
            80   85   90

Thr Leu Asp Ser Leu Pro Val Phe Gly Lys Val Val Thr Gln Gly
            95   100   105

Thr Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser Ser Ala Gly Val
            110   115   120

Ala Phe Ala Val Thr Arg Ala Cys Ser Ser Gly Glu Leu Glu Lys
125 130 135

Cys Gly Cys Asp Arg Thr Val His Gly Val Ser Pro Gln Gly Phe
140 145 150

Gln Trp Ser Gly Cys Ser Asp Asn Ile Ala Tyr Gly Val Ala Phe
155 160 165

Ser Gln Ser Phe Val Asp Val Arg Glu Arg Ser Lys Gly Ala Ser
170 175 180

Ser Ser Arg Ala Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg
185 190 195

Lys Ala Ile Leu Thr His Met Arg Val Glu Cys Lys Cys His Gly
200 205 210

Val Ser Gly Ser Cys Glu Val Lys Thr Cys Trp Arg Ala Val Pro
215 220 225

Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly
230 235 240

Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu
245 250 255

Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu
260 265 270

Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg
275 280 285

Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser
290 295 300

Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe
305 310 315

His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe
320 325 330

His Trp Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val
335 340 345

Glu Leu His Thr Cys Arg
350

<210> 227
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 227
gctgcagctg caaattccac tgg 23

<210> 228
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 228
tggtgggaga ctgtttaaat tatcggcc 28

<210> 229
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 229
tgcttcgtca agtgccggca gtgccagcgg ctcgtggagt t 41

<210> 230
<211> 1355
<212> DNA
<213> Homo sapiens

<400> 230
cggacgcgtg ggcggacgcg tgggcggacg cgtgggcgga cgcgtgggct 50

gggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcggca 100

gctccgagga ggtccccgga gggccctggg gacgctgggt gcactggagc 150

aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcctttg 200

ggctgtgatt ctgagtatcc tattgtccaa ggcctccacg gagcgcgcgg 250

cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300

gcggcgctgg gtgccctgaa ggaggaggtc ggagactgcc acagctgctg 350

ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400

cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450

cgcgtgaccc agggcttggc tgaagccggc aggggccgtg aggacgtccg 500

cactgagctg ttccgggcgc tggaggccgt gaggctccag aacaactcct 550

gcgagccgtg ccccacgtcg tggctgtcct tcgagggctc ctgctacttt 600

ttctctgtgc caaagacgac gtgggcggcg gcgcaggatc actgcgcaga 650

tgccagcgcg cacctggtga tcgttggggg cctggatgag cagggcttcc 700

tcactcggaa cacgcgtggc cgtggttact ggctgggcct gagggctgtg 750

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cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800

cagcttcagc cactggaacc agggagagcc caatgacgct tgggggcgcg 850

agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900

gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950

ccgcccagtg ccctggagcc gcgcccattg cagcatgtcg tatcctgggg 1000

gctgctcacc tccctggctc ctggagctga ttgccaaaga gtttttttct 1050

tcctcatcca ccgctgctga gtctcagaaa cacttggccc aacatagccc 1100

tgtccagccc agtgcctggg ctctgggacc tccatgccga cctcatccta 1150

actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200

ctcctgcgtc cccgtgatat gcctccactt ctctccctaa ccaaggttag 1250

gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300

gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350

aaaaa 1355

<210> 231
<211> 293
<212> PRT
<213> Homo sapiens

<400> 231
Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu
  1               5                  10                  15

Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg
                 20                  25                  30

Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp
                 35                  40                  45

Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg
                 50                  55                  60

Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser
                 65                  70                  75

Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp
                 80                  85                  90

Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr
                 95                 100                 105

Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu
                110                 115                 120

Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala
                125                 130                 135
```

Glu Ala Gly Arg Gly Arg Glu Asp Val Arg Thr Glu Leu Phe Arg
                140   145   150

Ala Leu Glu Ala Val Arg Leu Gln Asn Asn Ser Cys Glu Pro Cys
                155   160   165

Pro Thr Ser Trp Leu Ser Phe Glu Gly Ser Cys Tyr Phe Phe Ser
                170   175   180

Val Pro Lys Thr Thr Trp Ala Ala Ala Gln Asp His Cys Ala Asp
                185   190   195

Ala Ser Ala His Leu Val Ile Val Gly Gly Leu Asp Glu Gln Gly
                200   205   210

Phe Leu Thr Arg Asn Thr Arg Gly Arg Gly Tyr Trp Leu Gly Leu
                215   220   225

Arg Ala Val Arg His Leu Gly Lys Val Gln Gly Tyr Gln Trp Val
                230   235   240

Asp Gly Val Ser Leu Ser Phe Ser His Trp Asn Gln Gly Glu Pro
                245   250   255

Asn Asp Ala Trp Gly Arg Glu Asn Cys Val Met Met Leu His Thr
                260   265   270

Gly Leu Trp Asn Asp Ala Pro Cys Asp Ser Glu Lys Asp Gly Trp
                275   280   285

Ile Cys Glu Lys Arg His Asn Cys
                290

<210> 232
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 232
gcgagaactg tgtcatgatg ctgc 24

<210> 233
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 233
gtttctgaga ctcagcagcg gtgg 24

<210> 234
<211> 50
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 234
caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235
<211> 1847
<212> DNA
<213> Homo sapiens

<400> 235
gccaggggaa gagggtgatc cgacccgggg aaggtcgctg ggcagggcga 50

gttgggaaag cggcagcccc cgccgccccc gcagcccctt ctcctccttt 100

ctcccacgtc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150

agacaggagg aactggagcc tcattggccg gcccggggcg ccggcctcgg 200

gcttaaatag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250

cgctcccgct gctcctgccg ggtgatggaa aaccccagcc cggccgccgc 300

cctgggcaag gccctctgcg ctctcctcct ggccactctc ggcgccgccg 350

gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400

tacagcatca ccttcacggg caagtggagc cagacggcct tccccaagca 450

gtaccccctg ttccgccccc ctgcgcagtg gtcttcgctg ctgggggccg 500

cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550

gggctgcgcg actttgcgga gcgcggcgag gcctgggcgc tgatgaagga 600

gatcgaggcg gcgggggagg cgctgcagag cgtgcacgag gtgttttcgg 650

cgcccgccgt ccccagcggc accgggcaga cgtcggcgga gctggaggtg 700

cagcgcaggc actcgctggt ctcgtttgtg gtgcgcatcg tgcccagccc 750

cgactggttc gtgggcgtgg acagcctgga cctgtgcgac ggggaccgtt 800

ggcgggaaca ggcggcgctg gacctgtacc cctacgacgc cgggacggac 850

agcggcttca ccttctcctc ccccaacttc gccaccatcc cgcaggacac 900

ggtgaccgag ataacgtcct cctctcccag ccacccggcc aactccttct 950

actacccgcg gctgaaggcc ctgcctccca tcgccagggt gacactgctg 1000

cggctgcgac agagccccag ggccttcatc cctcccgccc cagtcctgcc 1050

cagcagggac aatgagattg tagacagcgc ctcagttcca gaaacgccgc 1100

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tggactgcga ggtctccctg tggtcgtcct ggggactgtg cggaggccac 1150

tgtgggaggc tcgggaccaa gagcaggact cgctacgtcc gggtccagcc 1200

cgccaacaac gggagcccct gccccgagct cgaagaagag gctgagtgcg 1250

tccctgataa ctgcgtctaa gaccagagcc ccgcagcccc tggggccccc 1300

cggagccatg gggtgtcggg ggctcctgtg caggctcatg ctgcaggcgg 1350

ccgagggcac aggggtttc gcgctgctcc tgaccgcggt gaggccgcgc 1400

cgaccatctc tgcactgaag ggccctctgg tggccggcac gggcattggg 1450

aaacagcctc ctcctttccc aaccttgctt cttaggggcc cccgtgtccc 1500

gtctgctctc agcctcctcc tcctgcagga taaagtcatc cccaaggctc 1550

cagctactct aaattatgtc tccttataag ttattgctgc tccaggagat 1600

tgtccttcat cgtccagggg cctggctccc acgtggttgc agatacctca 1650

gacctggtgc tctaggctgt gctgagccca ctctcccgag ggcgcatcca 1700

agcgggggcc acttgagaag tgaataaatg ggcggtttc ggaagcgtca 1750

gtgtttccat gttatggatc tctctgcgtt tgaataaaga ctatctctgt 1800

tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236
<211> 331
<212> PRT
<213> Homo sapiens

<400> 236
 Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys
   1               5                  10                  15

 Ala Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly
                  20                  25                  30

 Gly Glu Ser Ile Cys Ser Ala Arg Ala Pro Ala Lys Tyr Ser Ile
                  35                  40                  45

 Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr
                  50                  55                  60

 Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala
                  65                  70                  75

 Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val
                  80                  85                  90

 Ser Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala
                  95                 100                 105

 Leu Met Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val
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                    110                 115                 120

His Glu Val Phe Ser Ala Pro Ala Val Pro Ser Gly Thr Gly Gln
                125                 130                 135

Thr Ser Ala Glu Leu Glu Val Gln Arg Arg His Ser Leu Val Ser
                140                 145                 150

Phe Val Val Arg Ile Val Pro Ser Pro Asp Trp Phe Val Gly Val
                155                 160                 165

Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp Arg Glu Gln Ala
                170                 175                 180

Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly Phe
                185                 190                 195

Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val
                200                 205                 210

Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe
                215                 220                 225

Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr
                230                 235                 240

Leu Leu Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala
                245                 250                 255

Pro Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser
                260                 265                 270

Val Pro Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser
                275                 280                 285

Trp Gly Leu Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser
                290                 295                 300

Arg Thr Arg Tyr Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro
                305                 310                 315

Cys Pro Glu Leu Glu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys
                320                 325                 330

Val
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<210> 237
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 237
cagcactgcc aggggaagag gg 22

<210> 238
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 238
caggactcgc tacgtccg 18

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 239
cagccccttc tcctcctttc tccc 24

<210> 240
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 240
gcagttatca gggacgcact cagcc 25

<210> 241
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 241
ccagcgagag gcagatag 18

<210> 242
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 242
cggtcaccgt gtcctgcggg atg 23

<210> 243
<211> 42
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 243
cagccccttc tcctcctttc tcccacgtcc tatctgcctc tc 42

<210> 244
<211> 1894
<212> DNA
<213> Homo sapiens

<400> 244
ggcggcgtcc gtgaggggct cctttgggca ggggtagtgt ttggtgtccc 50

tgtcttgcgt gatattgaca aactgaagct ttcctgcacc actggactta 100

aggaagagtg tactcgtagg cggacagctt tagtggccgg ccggccgctc 150

tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200

tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250

gctggagata ttgacataga gttgtggtcc aaagaagctc ctaaagcttg 300

cagaaatttt atccaacttt gtttggaagc ttattatgac aataccattt 350

ttcatagagt tgtgcctggt ttcatagtcc aaggcggaga tcctactggc 400

acagggagtg gtggagagtc tatctatgga gcgccattca aagatgaatt 450

tcattcacgg ttgcgtttta atcggagagg actggttgcc atggcaaatg 500

ctggttctca tgataatggc agccagtttt tcttcacact gggtcgagca 550

gatgaactta acaataagca taccatcttt ggaaaggtta caggggatac 600

agtatataac atgttgcgac tgtcagaagt agacattgat gatgacgaaa 650

gaccacataa tccacacaaa ataaaaagct gtgaggtttt gtttaatcct 700

tttgatgaca tcattccaag ggaaattaaa aggctgaaaa aagagaaacc 750

agaggaggaa gtaaagaaat tgaaacccaa aggcacaaaa aattttagtt 800

tactttcatt tggagaggaa gctgaggaag aagaggagga agtaaatcga 850

gttagtcaga gcatgaaggg caaaagcaaa agtagtcatg acttgcttaa 900

ggatgatcca catctcagtt ctgttccagt tgtagaaagt gaaaaaggtg 950

atgcaccaga tttagttgat gatggagaag atgaaagtgc agagcatgat 1000

gaatatattg atggtgatga aaagaacctg atgagagaaa gaattgccaa 1050

aaaattaaaa aaggacacaa gtgcgaatgt taaatcagct ggagaaggag 1100 aagtggagaa gaaatcagtc agccgcagtg aagagctcag aaaagaagca 1150

agacaattaa aacgggaact cttagcagca aaacaaaaaa aagtagaaaa 1200

tgcagcaaaa caagcagaaa aaagaagtga agaggaagaa gcccctccag 1250

atggtgctgt tgccgaatac agaagagaaa agcaaaagta tgaagctttg 1300

aggaagcaac agtcaaagaa gggaacttcc cgggaagatc agacccttgc 1350

actgctgaac cagtttaaat ctaaactcac tcaagcaatt gctgaaacac 1400

ctgaaaatga cattcctgaa acagaagtag aagatgatga aggatggatg 1450

tcacatgtac ttcagtttga ggataaaagc agaaaagtga aagatgcaag 1500

catgcaagac tcagatacat ttgaaatcta tgatcctcgg aatccagtga 1550

ataaaagaag gagggaagaa agcaaaaagc tgatgagaga gaaaaaagaa 1600

agaagataaa atgagaataa tgataaccag aacttgctgg aaatgtgcct 1650

acaatggcct tgtaacagcc attgttccca acagcatcac ttaggggtgt 1700

gaaaagaagt atttttgaac ctgttgtctg gttttgaaaa acaattatct 1750

tgttttgcaa attgtggaat gatgtaagca aatgcttttg gttactggta 1800

catgtgtttt ttcctagctg accttttata ttgctaaatc tgaaataaaa 1850

taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245
<211> 472
<212> PRT
<213> Homo sapiens

<400> 245
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Met Ser Asn Ile Tyr Ile Gln Glu Pro Pro Thr Asn Gly Lys Val
  1               5                  10                  15

Leu Leu Lys Thr Thr Ala Gly Asp Ile Asp Ile Glu Leu Trp Ser
                 20                  25                  30

Lys Glu Ala Pro Lys Ala Cys Arg Asn Phe Ile Gln Leu Cys Leu
                 35                  40                  45

Glu Ala Tyr Tyr Asp Asn Thr Ile Phe His Arg Val Val Pro Gly
                 50                  55                  60

Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly
                 65                  70                  75

Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg
                 80                  85                  90

Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly
                 95                 100                 105
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Ser His Asp Asn Gly Ser Gln Phe Phe Phe Thr Leu Gly Arg Ala
                110                 115                 120

Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys Val Thr Gly
                125                 130                 135

Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp
                140                 145                 150

Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys Glu
                155                 160                 165

Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys
                170                 175                 180

Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys
                185                 190                 195

Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu
                200                 205                 210

Ala Glu Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met
                215                 220                 225

Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro
                230                 235                 240

His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala
                245                 250                 255

Pro Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp
                260                 265                 270

Glu Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile
                275                 280                 285

Ala Lys Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala
                290                 295                 300

Gly Glu Gly Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu
                305                 310                 315

Leu Arg Lys Glu Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala
                320                 325                 330

Lys Gln Lys Lys Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg
                335                 340                 345

Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr
                350                 355                 360

Arg Arg Glu Lys Gln Lys Tyr Glu Ala Leu Arg Lys Gln Gln Ser
                365                 370                 375

Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn
                380                 385                 390

Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu
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                   395                 400                 405

Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met
                410                 415                 420

Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp
                425                 430                 435

Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg
                440                 445                 450

Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met
                455                 460                 465

Arg Glu Lys Lys Glu Arg Arg
                470
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<210> 246
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 246
tgcggagatc ctactggcac aggg 24

<210> 247
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 247
cgagttagtc agagcatg 18

<210> 248
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 248
cagatggtgc tgttgccg 18

<210> 249
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 249
caactggaac aggaactgag atgtggatc 29

<210> 250
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 250
ctggttcagc agtgcaaggg tctg 24

<210> 251
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 251
cctctccgat taaaacgc 18

<210> 252
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 252
gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253
<211> 2456
<212> DNA
<213> Homo sapiens

<400> 253
cgccgccgtt ggggctggaa gttcccgcca ggtccgtgcc gggcgagaga 50

gatgctgccc ggcccgcctc ggctttgagg cgagagaagt gtcccagacc 100

catttcgcct tgctgacggc gtcgagccct ggccagacat gtccacaggg 150

ttctccttcg ggtccgggac tctgggctcc accaccgtgg ccgccggcgg 200

gaccagcaca ggcggcgttt tctccttcgg aacgggaacg tctagcaacc 250

cttctgtggg gctcaatttt ggaaatcttg gaagtacttc aactccagca 300

actacatctg ctccttcaag tggttttgga accgggctct ttggatctaa 350

acctgccact gggttcactc taggaggaac aaatacaggt gccttgcaca 400 ccaagaggcc tcaagtggtc accaaatatg gaaccctgca aggaaaacag 450

atgcatgtgg ggaagacacc catccaagtc tttttaggag tccccttctc 500

cagacctcct ctaggtatcc tcaggtttgc acctccagaa cccccggagc 550

cctggaaagg aatcagagat gctaccacct acccgcctgg atggagtctc 600

gctctgtcgc caggctggag tgcagtggca cgatctcggc tcactgcaac 650

ctccgcctcc cgggttcaag cgagtctcct gcctcagcct ctgagtgtct 700

ggggctacag gtgcctgcag gagtcctggg gccagctggc ctcgatgtac 750

gtcagcacgc gggaacggta caagtggctg cgcttcagcg aggactgtct 800

gtacctgaac gtgtacgcgc cggcgcgcgc gcccggggat ccccagctgc 850

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tcgtacgagg gctctgactt ggccgcccgc gagaaagtgg tgctggtgtt 950

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tgcccacctg gctggatgca accacaacag cacacagatc ctggtaaact 1300

gcctgagggc actatcaggg accaaggtga tgcgtgtgtc caacaagatg 1350

agattcctcc aactgaactt ccagagagac ccggaagaga ttatctggtc 1400

catgagccct gtggtggatg gtgtggtgat cccagatgac cctttggtgc 1450

tcctgaccca ggggaaggtt tcatctgtgc cctaccttct aggtgtcaac 1500

aacctggaat tcaattggct cttgccttat aatatcacca aggagcaggt 1550

accacttgtg gtggaggagt acctggacaa tgtcaatgag catgactgga 1600

agatgctacg aaaccgtatg atggacatag ttcaagatgc cactttcgtg 1650

tatgccacac tgcagactgc tcactaccac cgagaaaccc caatgatggg 1700

aatctgccct gctggccacg ctacaacaag gatgaaaagt acctgcagct 1750

ggattttacc acaagagtgg gcatgaagct caaggagaag aagatggctt 1800

tttggatgag tctgtaccag tctcaaagac ctgagaagca gaggcaattc 1850 taagggtggc tatgcaggaa ggagccaaag aggggtttgc ccccaccatc 1900

caggccctgg ggagactagc catggacata cctggggaca agagttctac 1950

ccaccccagt ttagaactgc aggagctccc tgctgcctcc aggccaaagc 2000

tagagctttt gcctgttgtg tgggacctgc actgcccttt ccagcctgac 2050

atcccatgat gcccctctac ttcactgttg acatccagtt aggccaggcc 2100

ctgtcaacac cacactgtgc tcagctctcc agcctcagga caacctcttt 2150

ttttcccttc ttcaaatcct cccacccttc aatgtctcct tgtgactcct 2200

tcttatggga ggtcgaccca gactgccact gcccctgtca ctgcacccag 2250

cttggcattt accatccatc ctgctcaacc ttgttcctgt ctgttcacat 2300

tggcctggag gcctagggca ggttgtgaca tggagcaaac ttttggtagt 2350

ttgggatctt ctctcccacc cacacttatc tcccccaggg ccactccaaa 2400

gtctatacac aggggtggtc tcttcaataa agaagtgttg attagaaaaa 2450

aaaaaa 2456

<210> 254
<211> 545
<212> PRT
<213> Homo sapiens

<400> 254
Met Ser Thr Gly Phe Ser Phe Gly Ser Gly Thr Leu Gly Ser Thr
1   5   10   15

Thr Val Ala Ala Gly Gly Thr Ser Thr Gly Gly Val Phe Ser Phe
            20   25   30

Gly Thr Gly Thr Ser Ser Asn Pro Ser Val Gly Leu Asn Phe Gly
            35   40   45

Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser
            50   55   60

Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly
            65   70   75

Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg
            80   85   90

Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
            95   100   105

His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe
            110   115   120

Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro
            125   130   135

Pro Glu Pro Trp Lys Gly Ile Arg Asp Ala Thr Thr Tyr Pro Pro
140 145 150

Gly Trp Ser Leu Ala Leu Ser Pro Gly Trp Ser Ala Val Ala Arg
155 160 165

Ser Arg Leu Thr Ala Thr Ser Ala Ser Arg Val Gln Ala Ser Leu
170 175 180

Leu Pro Gln Pro Leu Ser Val Trp Gly Tyr Arg Cys Leu Gln Glu
185 190 195

Ser Trp Gly Gln Leu Ala Ser Met Tyr Val Ser Thr Arg Glu Arg
200 205 210

Tyr Lys Trp Leu Arg Phe Ser Glu Asp Cys Leu Tyr Leu Asn Val
215 220 225

Tyr Ala Pro Ala Arg Ala Pro Gly Asp Pro Gln Leu Pro Val Met
230 235 240

Val Trp Phe Pro Gly Gly Ala Phe Ile Val Gly Ala Ala Ser Ser
245 250 255

Tyr Glu Gly Ser Asp Leu Ala Ala Arg Glu Lys Val Val Leu Val
260 265 270

Phe Leu Gln His Arg Leu Gly Ile Phe Gly Phe Leu Ser Thr Asp
275 280 285

Asp Ser His Ala Arg Gly Asn Trp Gly Leu Leu Asp Gln Met Ala
290 295 300

Ala Leu Arg Trp Val Gln Glu Asn Ile Ala Ala Phe Gly Gly Asp
305 310 315

Pro Gly Asn Val Thr Leu Phe Gly Gln Ser Ala Gly Ala Met Ser
320 325 330

Ile Ser Gly Leu Met Met Ser Pro Leu Ala Ser Gly Leu Phe His
335 340 345

Arg Ala Ile Ser Gln Ser Gly Thr Ala Leu Phe Arg Leu Phe Ile
350 355 360

Thr Ser Asn Pro Leu Lys Val Ala Lys Lys Val Ala His Leu Ala
365 370 375

Gly Cys Asn His Asn Ser Thr Gln Ile Leu Val Asn Cys Leu Arg
380 385 390

Ala Leu Ser Gly Thr Lys Val Met Arg Val Ser Asn Lys Met Arg
395 400 405

Phe Leu Gln Leu Asn Phe Gln Arg Asp Pro Glu Glu Ile Ile Trp
410 415 420

Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro

425 430 435

Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu
440 445 450

Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn
455 460 465

Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp
470 475 480

Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met
485 490 495

Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr
500 505 510

Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala
515 520 525

Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu
530 535 540

Pro Gln Glu Trp Ala
545

<210> 255
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 255
aggtgcctgc aggagtcctg ggg 23

<210> 256
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 256
ccacctcagg aagccgaaga tgcc 24

<210> 257
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 257
gaacggtaca agtggctgcg cttcagcgag gactgtctgt acctg 45

<210> 258
<211> 2764
<212> DNA
<213> Homo sapiens

<400> 258
gagaacaggc ctgtctcagg caggccctgc gcctcctatg cggagatgct 50

actgccactg ctgctgtcct cgctgctggg cgggtcccag gctatggatg 100

ggagattctg gatacgagtg caggagtcag tgatggtgcc ggagggcctg 150

tgcatctctg tgccctgctc tttctcctac ccccgacaag actggacagg 200

gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250

agggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300

acccggggcc gattccagct cactggggat cccgccaagg ggaactgctc 350

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gggtggagag aggaagctat gtgacatata atttcatgaa cgatgggttc 450

tttctaaaag taacagtgct cagcttcacg cccagacccc aggaccacaa 500

caccgacctc acctgccatg tggacttctc cagaaagggt gtgagcgcac 550

agaggaccgt ccgactccgt gtggcctatg cccccagaga ccttgttatc 600

agcatttcac gtgacaacac gccagccctg gagccccagc cccagggaaa 650

tgtcccatac ctggaagccc aaaaaggcca gttcctgcgg ctcctctgtg 700

ctgctgacag ccagcccccct gccacactga gctgggtcct gcagaacaga 750

gtcctctcct cgtcccatcc ctggggccct agacccctgg ggctggagct 800

gcccggggtg aaggctgggg attcagggcg ctacacctgc cgagcggaga 850

acaggcttgg ctcccagcag cgagccctgg acctctctgt gcagtatcct 900

ccagagaacc tgagagtgat ggtttcccaa gcaaacagga cagtcctgga 950

aaaccttggg aacggcacgt ctctcccagt actggagggc caaagcctgt 1000

gcctggtctg tgtcacacac agcagccccc cagccaggct gagctggacc 1050

cagaggggac aggttctgag cccctcccag ccctcagacc ccggggtcct 1100

ggagctgcct cgggttcaag tggagcacga aggagagttc acctgccacg 1150

ctcggcaccc actgggctcc cagcacgtct ctctcagcct ctccgtgcac 1200

tataagaagg gactcatctc aacggcattc tccaacggag cgtttctggg 1250

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cccctcctcc accaggtgct ccctccccag aatcaaagaa gaaccagaaa 1500

aagcagtatc agttgcccag tttcccagaa cccaaatcat ccactcaagc 1550

cccagaatcc caggagagcc aagaggagct ccattatgcc acgctcaact 1600

tcccaggcgt cagacccagg cctgaggccc ggatgcccaa gggcacccag 1650

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ctgggacttc ggctagggag gaaggtagag taagaggttg aagataacag 1750

agtgcaaagt ttccttctct ccctctctct ctctctttct ctctctctct 1800

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tcgggagttc gagaccagcc tggccaactt ggtgaaaccc cgtctctact 1950

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tttaaaccag agcaactcca tctggaatag gagctgaata aaatgaggct 2350

gagacctact gggctgcatt ctcagacagt ggaggcattc taagtcacag 2400

gatgagacag gaggtccgta caagatacag gtcataaaga ctttgctgat 2450

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gccacgagag tgacctctgg tcgtcctcac tgctacactc ctgacagcac 2550

catgacagtt tacaaatgcc atggcaacat caggaagtta cccgatatgt 2600

cccaaaaggg ggaggaatga ataatccacc ccttgtttag caaataagca 2650

agaaataacc ataaaagtgg gcaaccagca gctctaggcg ctgctcttgt 2700

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<210> 259
<211> 544
<212> PRT
<213> Homo sapiens

<400> 259

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                 20                  25                  30

Val Pro Glu Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr
                 35                  40                  45

Pro Arg Gln Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp
                 50                  55                  60

Phe Lys Ala Val Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr
                 65                  70                  75

Asn His Gln Ser Arg Glu Val Glu Met Ser Thr Arg Gly Arg Phe
                 80                  85                  90

Gln Leu Thr Gly Asp Pro Ala Lys Gly Asn Cys Ser Leu Val Ile
                 95                 100                 105

Arg Asp Ala Gln Met Gln Asp Glu Ser Gln Tyr Phe Phe Arg Val
                110                 115                 120

Glu Arg Gly Ser Tyr Val Thr Tyr Asn Phe Met Asn Asp Gly Phe
                125                 130                 135

Phe Leu Lys Val Thr Val Leu Ser Phe Thr Pro Arg Pro Gln Asp
                140                 145                 150

His Asn Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly
                155                 160                 165

Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro
                170                 175                 180

Arg Asp Leu Val Ile Ser Ile Ser Arg Asp Asn Thr Pro Ala Leu
                185                 190                 195

Glu Pro Gln Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys
                200                 205                 210

Gly Gln Phe Leu Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro
                215                 220                 225

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser
                230                 235                 240

His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val
                245                 250                 255
```

Lys Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg
260 265 270

Leu Gly Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro
275 280 285

Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val
290 295 300

Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly
305 310 315

Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser Pro Pro Ala
320 325 330

Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro Ser Gln
335 340 345

Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val Glu
350 355 360

His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser
365 370 375

Gln His Val Ser Leu Ser Leu Ser Val His Tyr Lys Lys Gly Leu
380 385 390

Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile
395 400 405

Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile
410 415 420

Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe
425 430 435

Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr
440 445 450

Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn
455 460 465

Ser Pro Arg Thr Pro Pro Pro Pro Gly Ala Pro Ser Pro Glu Ser
470 475 480

Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu
485 490 495

Pro Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu
500 505 510

Glu Leu His Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg
515 520 525

Pro Glu Ala Arg Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu
530 535 540

Val Lys Phe Gln

<210> 260
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 260
caaagcctgc gcctggtctg tg 22

<210> 261
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 261
ttctggagcc cagagggtgc tgag 24

<210> 262
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 262
ggagctgcca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263
<211> 2857
<212> DNA
<213> Homo sapiens

<400> 263
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actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttggag 100

caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150

ttgagagtga agcgtggctg ggtgtggaac caatttttg taccagagga 200

aatgaatacg actagtcatc acatcggcca gctaagatct gatttagaca 250

atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300

acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350

tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400

tcgctactgg aagggctgtg gaacctgagt ctgagtttgt catcaaagtt 450 tcggatatca atgacaatga accaaaattc ctagatgaac cttatgaggc 500

cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550

caagtgatgc tgacgatccc tcaagtggta ataatgctcg tctcctctac 600

agcttacttc aaggccagcc atatttttct gttgaaccaa caacaggagt 650

cataagaata tcttctaaaa tggatagaga actgcaagat gagtattggg 700

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gcagaaatgg attacagcat tgaagaggat gattcgcaaa catttgacat 950

tattactaat catgaaactc aagaaggaat agttatatta aaaaagaaag 1000

tggattttga gcaccagaac cactacggta ttagagcaaa agttaaaaac 1050

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ttccatatta tgtatttgaa gtttttgaag aaaccccaca gggatcattt 1200

gtaggcgtgg tgtctgccac agacccagac aataggaaat ctcctatcag 1250

gtattctatt actaggagca aagtgttcaa tatcaatgat aatggtacaa 1300

tcactacaag taactcactg gatcgtgaaa tcagtgcttg gtacaaccta 1350

agtattacag ccacagaaaa atacaatata gaacagatct cttcgatccc 1400

actgtatgtg caagttctta acatcaatga tcatgctcct gagttctctc 1450

aatactatga gacttatgtt tgtgaaaatg caggctctgg tcaggtaatt 1500

cagactatca gtgcagtgga tagagatgaa tccatagaag agcaccattt 1550

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ctttccatgg gattcaagac agaagttatc attgctattc tcatttgcat 1850

tatgatcata tttgggttta ttttttgac tttgggttta aaacaacgga 1900 gaaaacagat tctatttcct gagaaaagtg aagatttcag agagaatata 1950

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tatagcagag ctgaggagta gtaccataat gcgggaacgc aagactcgga 2050

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ggccccgaca gtgccatatt caggaaattc attctggaaa agctcgaaga 2150

agctaatact gatccgtgtg cccctccttt tgattccctc cagacctacg 2200

cttttgaggg aacagggtca ttagctggat ccctgagctc cttagaatca 2250

gcagtctctg atcaggatga aagctatgat taccttaatg agttgggacc 2300

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tatagtcaga gaaattttca tgaattattc catgaagtat tgtttccttt 2850

atttaaa 2857

<210> 264
<211> 772
<212> PRT
<213> Homo sapiens

<400> 264
Met Asn Cys Tyr Leu Leu Leu Arg Phe Met Leu Gly Ile Pro Leu
1   5   10   15

Leu Trp Pro Cys Leu Gly Ala Thr Glu Asn Ser Gln Thr Lys Lys
                20   25   30

Val Lys Gln Pro Val Arg Ser His Leu Arg Val Lys Arg Gly Trp
                35   40   45

Val Trp Asn Gln Phe Phe Val Pro Glu Glu Met Asn Thr Thr Ser
                50   55   60

```
His His Ile Gly Gln Leu Arg Ser Asp Leu Asp Asn Gly Asn Asn
                 65                  70                  75

Ser Phe Gln Tyr Lys Leu Leu Gly Ala Gly Ala Gly Ser Thr Phe
                 80                  85                  90

Ile Ile Asp Glu Arg Thr Gly Asp Ile Tyr Ala Ile Gln Lys Leu
                 95                 100                 105

Asp Arg Glu Glu Arg Ser Leu Tyr Ile Leu Arg Ala Gln Val Ile
                110                 115                 120

Asp Ile Ala Thr Gly Arg Ala Val Glu Pro Glu Ser Glu Phe Val
                125                 130                 135

Ile Lys Val Ser Asp Ile Asn Asp Asn Glu Pro Lys Phe Leu Asp
                140                 145                 150

Glu Pro Tyr Glu Ala Ile Val Pro Glu Met Ser Pro Glu Gly Thr
                155                 160                 165

Leu Val Ile Gln Val Thr Ala Ser Asp Ala Asp Asp Pro Ser Ser
                170                 175                 180

Gly Asn Asn Ala Arg Leu Leu Tyr Ser Leu Leu Gln Gly Gln Pro
                185                 190                 195

Tyr Phe Ser Val Glu Pro Thr Thr Gly Val Ile Arg Ile Ser Ser
                200                 205                 210

Lys Met Asp Arg Glu Leu Gln Asp Glu Tyr Trp Val Ile Ile Gln
                215                 220                 225

Ala Lys Asp Met Ile Gly Gln Pro Gly Ala Leu Ser Gly Thr Thr
                230                 235                 240

Ser Val Leu Ile Lys Leu Ser Asp Val Asn Asp Asn Lys Pro Ile
                245                 250                 255

Phe Lys Glu Ser Leu Tyr Arg Leu Thr Val Ser Glu Ser Ala Pro
                260                 265                 270

Thr Gly Thr Ser Ile Gly Thr Ile Met Ala Tyr Asp Asn Asp Ile
                275                 280                 285

Gly Glu Asn Ala Glu Met Asp Tyr Ser Ile Glu Glu Asp Asp Ser
                290                 295                 300

Gln Thr Phe Asp Ile Ile Thr Asn His Glu Thr Gln Glu Gly Ile
                305                 310                 315

Val Ile Leu Lys Lys Lys Val Asp Phe Glu His Gln Asn His Tyr
                320                 325                 330

Gly Ile Arg Ala Lys Val Lys Asn His His Val Pro Glu Gln Leu
                335                 340                 345

Met Lys Tyr His Thr Glu Ala Ser Thr Thr Phe Ile Lys Ile Gln
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                    350                 355                 360

Val Glu Asp Val Asp Glu Pro Pro Leu Phe Leu Leu Pro Tyr Tyr
                365                 370                 375

Val Phe Glu Val Phe Glu Glu Thr Pro Gln Gly Ser Phe Val Gly
                380                 385                 390

Val Val Ser Ala Thr Asp Pro Asp Asn Arg Lys Ser Pro Ile Arg
                395                 400                 405

Tyr Ser Ile Thr Arg Ser Lys Val Phe Asn Ile Asn Asp Asn Gly
                410                 415                 420

Thr Ile Thr Thr Ser Asn Ser Leu Asp Arg Glu Ile Ser Ala Trp
                425                 430                 435

Tyr Asn Leu Ser Ile Thr Ala Thr Glu Lys Tyr Asn Ile Glu Gln
                440                 445                 450

Ile Ser Ser Ile Pro Leu Tyr Val Gln Val Leu Asn Ile Asn Asp
                455                 460                 465

His Ala Pro Glu Phe Ser Gln Tyr Tyr Glu Thr Tyr Val Cys Glu
                470                 475                 480

Asn Ala Gly Ser Gly Gln Val Ile Gln Thr Ile Ser Ala Val Asp
                485                 490                 495

Arg Asp Glu Ser Ile Glu Glu His His Phe Tyr Phe Asn Leu Ser
                500                 505                 510

Val Glu Asp Thr Asn Asn Ser Ser Phe Thr Ile Ile Asp Asn Gln
                515                 520                 525

Asp Asn Thr Ala Val Ile Leu Thr Asn Arg Thr Gly Phe Asn Leu
                530                 535                 540

Gln Glu Glu Pro Val Phe Tyr Ile Ser Ile Leu Ile Ala Asp Asn
                545                 550                 555

Gly Ile Pro Ser Leu Thr Ser Thr Asn Thr Leu Thr Ile His Val
                560                 565                 570

Cys Asp Cys Gly Asp Ser Gly Ser Thr Gln Thr Cys Gln Tyr Gln
                575                 580                 585

Glu Leu Val Leu Ser Met Gly Phe Lys Thr Glu Val Ile Ile Ala
                590                 595                 600

Ile Leu Ile Cys Ile Met Ile Ile Phe Gly Phe Ile Phe Leu Thr
                605                 610                 615

Leu Gly Leu Lys Gln Arg Arg Lys Gln Ile Leu Phe Pro Glu Lys
                620                 625                 630

Ser Glu Asp Phe Arg Glu Asn Ile Phe Gln Tyr Asp Asp Glu Gly
                635                 640                 645
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Gly Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile Ala Glu Leu Arg
                650                 655                 660

Ser Ser Thr Ile Met Arg Glu Arg Lys Thr Arg Lys Thr Thr Ser
                665                 670                 675

Ala Glu Ile Arg Ser Leu Tyr Arg Gln Ser Leu Gln Val Gly Pro
                680                 685                 690

Asp Ser Ala Ile Phe Arg Lys Phe Ile Leu Glu Lys Leu Glu Glu
                695                 700                 705

Ala Asn Thr Asp Pro Cys Ala Pro Pro Phe Asp Ser Leu Gln Thr
                710                 715                 720

Tyr Ala Phe Glu Gly Thr Gly Ser Leu Ala Gly Ser Leu Ser Ser
                725                 730                 735

Leu Glu Ser Ala Val Ser Asp Gln Asp Glu Ser Tyr Asp Tyr Leu
                740                 745                 750

Asn Glu Leu Gly Pro Arg Phe Lys Arg Leu Ala Cys Met Phe Gly
                755                 760                 765

Ser Ala Val Gln Ser Asn Asn
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<210> 265
<211> 349
<212> DNA
<213> Homo sapiens

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<221> unsure
<222> 24, 60, 141, 226, 228, 249, 252
<223> unknown base

<400> 265
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 gaatattttn taaaatggat agagaactgc aagatgagta ttgggtaatc 100

 attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150

 aagtgtatta attaaacttt cagatgttaa tgacaataag cctatattta 200

 aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250

 tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300

 aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
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<223> Synthetic oligonucleotide probe

<400> 266
cttgactgtc tctgaatctg caccc 25

<210> 267
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 267
aagtggtgga agcctccagt gtgg 24

<210> 268
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 268
ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 269
<211> 2747
<212> DNA
<213> Homo sapiens

<400> 269
gcaacctcag cttctagtat ccagactcca gcgccgcccc gggcgcggac 50

cccaaccccg acccagagct tctccagcgg cggcgcagcg agcagggctc 100

cccgccttaa cttcctccgc ggggcccagc caccttcggg agtccgggtt 150

gcccacctgc aaactctccg ccttctgcac ctgccacccc tgagccagcg 200

cgggcccccg agcgagtcat ggccaacgcg gggctgcagc tgttgggctt 250

cattctcgcc ttcctgggat ggatcggcgc catcgtcagc actgccctgc 300

cccagtggag gatttactcc tatgccggcg acaacatcgt gaccgcccag 350

gccatgtacg aggggctgtg gatgtcctgc gtgtcgcaga gcaccgggca 400

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atctttgtgg ccaccgttgg catgaagtgt atgaagtgct tggaagacga 550

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gttcaagaat tctatgaccc tatgacccca gtcaatgcca ggtacgaatt 700

tggtcaggct ctcttcactg gctgggctgc tgcttctctc tgccttctgg 750

gaggtgccct actttgctgt tcctgtcccc gaaaaacaac ctcttaccca 800

acaccaaggc cctatccaaa acctgcacct tccagcggga aagactacgt 850

gtgacacaga ggcaaaagga gaaaatcatg ttgaaacaaa ccgaaaatgg 900

acattgagat actatcatta acattaggac cttagaattt tgggtattgt 950

aatctgaagt atggtattac aaaacaaaca aacaaacaaa aaacccatgt 1000

gttaaaatac tcagtgctaa acatggctta atcttatttt atcttctttc 1050

ctcaatatag gagggaagat tttccattt gtattactgc ttcccattga 1100

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gtttctaaag ccaagaagaa tttattacaa atcagaactt tggaggcaaa 1600

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gattgaattt ttaagctact tattcatagt tttatatccc cctaaactac 1800

ctttttgttc cccattcctt aattgtattg ttttcccaag tgtaattatc 1850

atgcgtttta tatcttccta ataaggtgtg gtctgtttgt ctgaacaaag 1900

tgctagactt tctggagtga taatctggtg acaaatattc tctctgtagc 1950

tgtaagcaag tcacttaatc tttctacctc ttttttctat ctgccaaatt 2000

gagataatga tacttaacca gttagaagag gtagtgtgaa tattaattag 2050

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acacgtacct tcatgtgatt cactgccttc ctctctctac cagtctattt 2200

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gatgttgtgg ggatccagtg agatagaata catgtaagtg tggttttgta 2650

atttaaaaag tgctatacta agggaaagaa ttgaggaatt aactgcatac 2700

gttttggtgt tgcttttcaa atgtttgaaa ataaaaaaaa tgttaag 2747

<210> 270
<211> 211
<212> PRT
<213> Homo sapiens

<400> 270
Met Ala Asn Ala Gly Leu Gln Leu Leu Gly Phe Ile Leu Ala Phe
 1               5                   10                  15

Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp
            20                  25                  30

Arg Ile Tyr Ser Tyr Ala Gly Asp Asn Ile Val Thr Ala Gln Ala
            35                  40                  45

Met Tyr Glu Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly
            50                  55                  60

Gln Ile Gln Cys Lys Val Phe Asp Ser Leu Leu Asn Leu Ser Ser
            65                  70                  75

Thr Leu Gln Ala Thr Arg Ala Leu Met Val Val Gly Ile Leu Leu
            80                  85                  90

Gly Val Ile Ala Ile Phe Val Ala Thr Val Gly Met Lys Cys Met
            95                  100                 105

Lys Cys Leu Glu Asp Asp Glu Val Gln Lys Met Arg Met Ala Val
           110                  115                 120
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Ile Gly Gly Ala Ile Phe Leu Leu Ala Gly Leu Ala Ile Leu Val
                125                 130                 135

Ala Thr Ala Trp Tyr Gly Asn Arg Ile Val Gln Glu Phe Tyr Asp
                140                 145                 150

Pro Met Thr Pro Val Asn Ala Arg Tyr Glu Phe Gly Gln Ala Leu
                155                 160                 165

Phe Thr Gly Trp Ala Ala Ala Ser Leu Cys Leu Leu Gly Gly Ala
                170                 175                 180

Leu Leu Cys Cys Ser Cys Pro Arg Lys Thr Thr Ser Tyr Pro Thr
                185                 190                 195

Pro Arg Pro Tyr Pro Lys Pro Ala Pro Ser Ser Gly Lys Asp Tyr
                200                 205                 210

Val


<210> 271
<211> 564
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 21, 69, 163, 434, 436, 444
<223> unknown base

<400> 271
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ggatggatcg gcgccatcnt cacactgccc ttccccagtg gaggatttta 100

ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150

ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200

ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250

tgatggtggt tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300

gttggcatga agtgtatgaa gtgcttggaa gacgatgagg tgcagaagat 350

gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400

ttttagttgc cacagcatgg tatggcaata gaancnttca acanttctat 450

gaccctatga ccccagtcaa tgccaggtac gaatttggtc aggctctctt 500

cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550

gctgttcctg tccc 564

<210> 272
<211> 498
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<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341
<223> unknown base

<400> 272
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tccagctgtt gggcttcatt ctccccttcc tgggatggac cggcgcccat 100

cntcagcact gccctgcccc agtggaggat ttactcctat nccggcnaca 150

acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtcctgcgtg 200

tcgcagagca ccgggcagat ccagtgcaaa gtctttgact cccttgctga 250

atctgagcag cacattgcaa gcaacccgtg ccttgatggt ggttggcatc 300

ctcctgggag tgatagcaat cttnntggcc accgttgtnn ntgaagtgta 350

tgaagtgctt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400

gggggcgcga tatttcttct tgcaggtctg gctattttag ttgccacagc 450

atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273
<211> 552
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394
<223> unknown base

<400> 273
gggcccgacc attatccaac cgggntcact gttggctcat ctccctcctg 50

gatgaancgc gccatcntca gactccctgc cccatggaga tttnncctat 100

gctggcgaca acatcntgac ccccagccat gtacgagggg ctttgaacgt 150

cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200

tgctgaatct gngcagcaca ttgcagcaac ccntgccctg atggtggttg 250

gcatcctcct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300

tgtatgaagt gcttggaaga cgatgaggtg cagaagatga ggatggctgt 350

cattgggggc gcgatatttc ttcttgcagg tctggctatt tnnngttgcc 400

acagcatggt atggcaatag aatcgttcaa gaattctatg accctatgac 450 cccagtcaat gccaggtacg aatttggtca ggctctcttc actggctggg 500

ctgctgcttc tctctgcctt ctgggaggtg ccctactttg ctgttcctgc 550

ga 552

<210> 274
<211> 526
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407
<223> unknown base

<400> 274
attctcccct cctggatgga tcgcnccacc gtcacattgc cttcccccan 50

tggaggattn actcctatgc tggcgacaac atcgtgaccc cccaggccat 100

ttaccgaggg gctttggatg tcntgcntgt cgcagagcac cgggcagatc 150

ccagtgcaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200

caacccgtgc cttgatgggg ttggcatcct cctgggagtg atagcaacct 250

ttgtggccac cgttggcatg aagtgtatga agtgcttgga agacgatgag 300

gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttgttg 350

caggtctggc tattttagtn gccacagcat ggtatggcaa tagantnntt 400

cnngnnntct atgaccctat gaccccagtc aatgccaggt acgaatttgg 450

tcaggctctc ttcactggct gggctgctgc ttctctctgc cttctgggag 500

gtgccctact ttgctgttcc tgtccc 526

<210> 275
<211> 398
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274
<223> unknown base

<400> 275
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gcagcacatt ncaagcaacc ccttgccttg aaggtggttg ncatcccccc 100

tgggagtgaa tagcaatctt tgtggccacc gttggcatga agtntatgaa 150

gtgcttggaa gacgatgagg tgcagaagat gaggatggct gtcattgggg 200 gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250

tatggcaata gnatnnttcg nggnttctat gaccctatga ccccagtcaa 300

tgccaggtac gaatttggtc aggctctctt cactggctgg gctgctgctt 350

ctctctgcct tctgggaggt gccctacttt gctgttcctg tccccgaa 398

<210> 276
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476
<223> unknown base

<400> 276
agcaatgccc tgcccccagt ggaggattaa ttcctatgnt ggggacaaca 50

ttgtgacngc ccaggccatg tacgggggc tgtggatgtc ctgcgtgtcg 100

cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150

gagcagcaca ttgcaagcaa cccgtgcctt gatggtggtt ggcatcttcc 200

tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250

tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300

cgcgatattt cttnttgcag gtctggctat tttagttgcc acagcatggt 350

atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400

gccaggtacg aatttggtca ggctttnttc actggctggg ctgctgcttn 450

tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277
<211> 200
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 34, 87, 138, 147, 163, 165-166, 172
<223> unknown base

<400> 277
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cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100

ccccagtcaa tgccaggtac gaatttggtc aggctctntt cactggntgg 150

gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcctg 200

<210> 278
<211> 542
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396
<223> unknown base

<400> 278
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ttacncctat gctggcgaac aacatcntga ccgcccaggc catgtacgag 100

gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtgca 150

aagtctttga ctccttgctg aatctgagca gcacattgca agcaaccntg 200

ccttgatggt ggttggcatc ctcctgggag tgatagcaat ctttgtggcc 250

accgttggca tgaaagtgta tgaagtgctt ggaagacgat gaggtgcaga 300

agatgaggat ggctgtcatt gggggcgcga tatttcttct tgcaggtctg 350

gctattttag nngccacagc atggtatggc aatcagaccc nntcanaaac 400

tctatgaccc tatgacccca gtcaatgcca ggtacgaatt tggtcaggct 450

ctcttcactg gctgggctgc tgcttctctc tgccttctgg gaggtgccct 500

actttgctgt tcctgtcccc gaaaaacaac ctcttaccca cg 542

<210> 279
<211> 548
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 90, 115, 147, 228, 387
<223> unknown base

<400> 279
cggggctgca gctgttgggc ttcatctcgc ttcctgggat ggaatcggcg 50

ccatcgtcag cactgccctg ccccatggag gatttactcn tatgctggcg 100

acaacatcgt gaccncccag gccatgtacg aggggctgtg gatgtcngcg 150

tgtcgcagag caccgggcag atccagtgca aagtctttga ctccttgctg 200

aatctgagca gcacattgca agcaaccntg ccttgatggt ggttggcatc 250

ctcctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300

gaagtgcttg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350 gggcgcgat atttcttctt gcaggtctgg ctatttntag ttgccacagc 400

atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450

tcaatgccag gtacgaattt ggtcaggctc tcttcactgg ctgggctgct 500

gcttctctct gccttctggg aggtgcccta ctttgctgtt cctgcgaa 548

<210> 280
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
cgagcgagtc atggccaacg c 21

<210> 281
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 281
gtgtcacacg tagtctttcc cgctgg 26

<210> 282
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 282
ctgcagctgt tgggcttcat tctcgccttc ctgggatgga tcg 43

<210> 283
<211> 2285
<212> DNA
<213> Homo sapiens

<400> 283
gcgtgccgtc agctcgccgg gcaccgcggc ctcgccctcg ccctccgccc 50

ctgcgcctgc accgcgtaga ccgacccccc cctccagcgc gcccacccgg 100

tagaggaccc ccgcccgtgc cccgaccggt ccccgccttt ttgtaaaact 150

taaagcgggc gcagcattaa cgcttcccgc cccggtgacc tctcaggggt 200

ctccccgcca aaggtgctcc gccgctaagg aacatggcga aggtggagca 250

ggtcctgagc ctcgagccgc agcacgagct caaattccga ggtcccttca 300 ccgatgttgt caccaccaac ctaaagcttg gcaacccgac agaccgaaat 350

gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400

caacagcgga atcatcgatg caggggcctc aattaatgta tctgtgatgt 450

tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500

gttcagtcta tgtttgctcc aactgacact tcagatatgg aagcagtatg 550

gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600

ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650

attatatcca caactgcatc aaagacagaa acaccaatag tgtctaagtc 700

tctgagttct tctttggatg acaccgaagt taagaaggtt atggaagaat 750

gtaagaggct gcaaggtgaa gttcagaggc tacgggagga gaacaagcag 800

ttcaaggaag aagatggact gcggatgagg aagacagtgc agagcaacag 850

ccccatttca gcattagccc caactgggaa ggaagaaggc cttagcaccc 900

ggctcttggc tctggtggtt ttgttcttta tcgttggtgt aattattggg 950

aagattgcct tgtagaggta gcatgcacag gatggtaaat tggattggtg 1000

gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050

aattaatgta tgatgacatc tcacaggtct tgcctttaaa ttacccctcc 1100

ctgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150

ttagaaagtt aaaaatgtat agtaactgat tgagggggaa aaagaatgat 1200

ctttattaat gacaagggaa accatgagta atgccacaat ggcatattgt 1250

aaatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300

tctcttaaaa tgacaccctt cctcgcctgt tggtgctggc ccttggggag 1350

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aagccatcag ctccttggga ctgatgaaca gagtcagaag cccaaaggaa 1500

ttgcactgtg gcagcatcag acgtactcgt cataagtgag aggcgtgtgt 1550

tgactgattg acccagcgct ttggaaataa atggcagtgc tttgttcact 1600

taaagggacc aagctaaatt tgtattggtt catgtagtga agtcaaactg 1650

ttattcagag atgtttaatg catatttaac ttatttaatg tatttcatct 1700

catgttttct tattgtcaca agagtacagt taatgctgcg tgctgctgaa 1750 ctctgttggg tgaactggta ttgctgctgg agggctgtgg gctcctctgt 1800

ctctggagag tctggtcatg tggaggtggg gtttattggg atgctggaga 1850

agagctgcca ggaagtgttt tttctgggtc agtaaataac aactgtcata 1900

gggagggaaa ttctcagtag tgacagtcaa ctctaggtta cctttttttaa 1950

tgaagagtag tcagtcttct agattgttct tataccacct ctcaaccatt 2000

actcacactt ccagcgccca ggtccaagtc tgagcctgac ctccccttgg 2050

ggacctagcc tggagtcagg acaaatggat cgggctgcag agggttagaa 2100

gcgagggcac cagcagttgt gggtggggag caagggaaga gagaaactct 2150

tcagcgaatc cttctagtac tagttgagag tttgactgtg aattaatttt 2200

atgccataaa agaccaaccc agttctgttt gactatgtag catcttgaaa 2250

agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284
<211> 243
<212> PRT
<213> Homo sapiens

<400> 284
Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu
1   5   10   15

Leu Lys Phe Arg Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu
            20   25   30

Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys
            35   40   45

Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile
            50   55   60

Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro
            65   70   75

Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val
            80   85   90

Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val
            95   100   105

Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg
            110   115   120

Cys Val Phe Glu Leu Pro Ala Glu Asn Asp Lys Pro His Asp Val
            125   130   135

Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr
            140   145   150

```
Pro Ile Val Ser Lys Ser Leu Ser Ser Ser Leu Asp Asp Thr Glu
                155                 160                 165

Val Lys Lys Val Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Val
                170                 175                 180

Gln Arg Leu Arg Glu Glu Asn Lys Gln Phe Lys Glu Glu Asp Gly
                185                 190                 195

Leu Arg Met Arg Lys Thr Val Gln Ser Asn Ser Pro Ile Ser Ala
                200                 205                 210

Leu Ala Pro Thr Gly Lys Glu Glu Gly Leu Ser Thr Arg Leu Leu
                215                 220                 225

Ala Leu Val Val Leu Phe Phe Ile Val Gly Val Ile Ile Gly Lys
                230                 235                 240

Ile Ala Leu
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<210> 285
<211> 418
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 40, 53, 68, 119, 134, 177-178, 255
<223> unknown base

<400> 285
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tcnagcgccc aggtccangt ctgagcctga cttcccсttg gggacctagc 100

ctggagtcag gacaatggnt cgggctgcag aggnttagaa gcgagggcac 150

cagcagtttt gggtggggag caagggnnga gagaaactct tcagcgaatc 200

cttctagtac tagttgagag tttgactgtg aattaatttt atgccataaa 250

agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300

taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350

ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400

gttaacttta aaatgagc 418
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<210> 286
<211> 543
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 73, 97

<223> unknown base

<400> 286
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gattacctcc ttaaatgaca ccnttcctcg cctgttggtg ctggccnttg 100

gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150

gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200

ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250

aaggaattgc cactgtggca gcatcagacg tactcgtcat aagtgagagg 300

cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcttt 350

gttcacttaa agggaccaag ctaaattgta ttggttcatg tagtgaagtc 400

aaactgttat tcagagatgt ttaatgcata tttaacttat ttaatgtatt 450

tcatctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500

gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287
<211> 270
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242
<223> unknown base

<400> 287
ccctggtggt tttgttcttt aattcgttgg tgtaattntt gggaagattg 50

cttgtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100

catatccatg ggatttaaat ttatcataac catgtgtaaa aagaaattaa 150

tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200

acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250

agttaaaaat gtatagtaac 270

<210> 288
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 35, 116, 129, 197, 278, 294, 297, 349, 351
<223> unknown base

<400> 288
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gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100

gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150

actgattgac ccagcgcttt ggaaataaat ggcagtgctt tgttcantta 200

aagggaccaa gctaaatttg tattggttca tgtagtgaag tcaaactgtt 250

attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300

tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350

ntgttgggtg aactggtatt gctgctggag ggctgtgggc tcctctgtct 400

ttggagagtc tggtcatgtg gaggtggg 428

<210> 289
<211> 320
<212> DNA
<213> Homo sapiens

<400> 289
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atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100

tactcgtcat aagtgagagg cgtgtgttga ctgattgacc cagcgctttg 150

gaaataaatg gcagtgcttt gttcacttaa agggaccaag ctaaatttgt 200

attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250

atttaactta tttaatgtat ttcatctcat gttttcttat tgtcacaaga 300

gtacagttaa tgctgcgtgc 320

<210> 290
<211> 609
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
447, 481, 513, 532, 584, 598
<223> unknown base

<400> 290
aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50

gaaaccntgn gtaatgccac aatggcatat tgtaaatgtc attttaaaca 100

ttggtaggcc ttggtacatg atgctggatt acctctctta aaatgacacc 150

cttcctcgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200 ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantcccgg 250

cccaggctgc tttccgtgtc ttcagttctg tccaagccat cagctccttg 300

ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350

cagangtant ngtcataagt gagaggcgtg tgttgantga ttgacccagc 400

gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450

atttgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500

atgcatattt aanttattta atgtatttca tntcatgttt tcttattgtc 550

acaagggtac agttaatgct gcgtgctgct gaantctgtt gggtgaantg 600

gtattgctg 609

<210> 291
<211> 493
<212> DNA
<213> Homo sapiens

<400> 291
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cacagtagtc cccacgtggc ccactcccgg cccaggctgc tttccgtgtc 100

ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150

aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200

gagaggcgtg tgttgactga ttgacccagc gctttggaaa taaatggcag 250

tgctttgttc acttaaaggg accaagctaa atttgtattg gttcatgtag 300

tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350

atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400

gcgtgctgct gaactctgtt gggtgaactg gtattgctgc tggagggctg 450

tgggctcctc tgtctctgga gagtctggtc atgtggaggt ggg 493

<210> 292
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 292
gcaccaccgt aggtacttgt gtgaggc 27

<210> 293
<211> 23
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 293
aaccaccaga gccaagagcc ggg 23

<210> 294
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 294
cagcggaatc atcgatgcag ggcctcaat taatgtatct gtgatgttac 50

<210> 295
<211> 2530
<212> DNA
<213> Homo sapiens

<400> 295
gcgagctccg ggtgctgtgg cccggccttg gcggggcggc ctccggctca 50

ggctggctga gaggctccca gctgcagcgt ccccgcccgc ctcctcggga 100

gctctgatct cagctgacag tgccctcggg gaccaaacaa gcctggcagg 150

gtctcacttt gttgcccagg ctggagttca gtgccatgat catggtttac 200

tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250

acaggacaaa attagaagat caaaatggaa aatatgctgc tttggttgat 300

atttttcacc cctgggtgga ccctcattga tggatctgaa atggaatggg 350

attttatgtg gcacttgaga aaggtacccc ggattgtcag tgaaaggact 400

ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450

tacagtgtgt ggcatcgaat gccagaaaga actcccaact cccagccttt 500

ctgaattgga ggattatctt tcctatgaga ctgtctttga gaatggcacc 550

cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccgactca 600

aaatatcacc acaaagggag tatctgttag gagaaagaga caggtgtatg 650

gcaccgacag caggttcagc atcttggaca aaaggttctt aaccaatttc 700

cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcattctcat 750

ttcccctcag catgttctaa ctgctgccca ctgtgttcat gatggaaagg 800

actatgtcaa agggagtaaa aagctaaggg tagggttgtt gaagatgagg 850 aataaaagtg gaggcaagaa acgtcgaggt tctaagagga gcaggagaga 900

agctagtggt ggtgaccaaa gagagggtac cagagagcat ctgcaggaga 950

gagcgaaggg tgggagaaga agaaaaaaat ctggccgggg tcagaggatt 1000

gccgaaggga ggccttcctt tcagtggacc cgggtcaaga atacccacat 1050

tccgaagggc tgggcacgag gaggcatggg ggacgctacc ttggactatg 1100

actatgctct tctggagctg aagcgtgctc acaaaaagaa atacatggaa 1150

cttggaatca gcccaacgat caagaaaatg cctggtggaa tgatccactt 1200

ctcaggattt gataacgata gggctgatca gttggtctat cggttttgca 1250

gtgtgtccga cgaatccaat gatctccttt accaatactg cgatgctgag 1300

tcgggctcca ccggttcggg ggtctatctg cgtctgaaag atccagacaa 1350

aaagaattgg aagcgcaaaa tcattgcggt ctactcaggg caccagtggg 1400

tggatgtcca cggggttcag aaggactaca acgttgctgt tcgcatcact 1450

cccctaaaat acgcccagat ttgcctctgg attcacggga acgatgccaa 1500

ttgtgcttac ggctaacaga gacctgaaac agggcggtgt atcatctaaa 1550

tcacagagaa aaccagctct gcttaccgta gtgagatcac ttcataggtt 1600

atgcctggac ttgaactctg tcaatagcat ttcaacattt ttcaaaatca 1650

ggagattttc gtccatttaa aaaatgtata ggtgcagata ttgaaactag 1700

gtgggcactt caatgccaag tatatactct tctttacatg gtgatgagtt 1750

tcatttgtag aaaaattttg ttgccttctt aaaaattaga cacactttaa 1800

accttcaaac aggtattata aataacatgt gactccttaa tggacttatt 1850

ctcagggtcc tactctaaga agaatctaat aggatgctgg ttgtgtatta 1900

aatgtgaaat tgcatagata aaggtagatg gtaaagcaat tagtatcaga 1950

atagagacag aaagttacaa cacagtttgt actactctga gatggatcca 2000

ttcagctcat gccctcaatg tttatattgt gttatctgtt gggtctggga 2050

catttagttt agtttttttg aagaattaca aatcagaaga aaaagcaagc 2100

attataaaca aaactaataa ctgttttact gctttaagaa ataacaatta 2150

caatgtgtat tatttaaaaa tgggagaaat agtttgttct atgaaataaa 2200

cctagtttag aaatagggaa gctgagacat tttaagatct caagttttta 2250

tttaactaat actcaaaata tggacttttc atgtatgcat agggaagaca 2300 cttcacaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350

atacattcta tgtatgaggt gctacatttt taggacaaag aattctgtaa 2400

tctttttcaa gaaagagtct ttttctcctt gacaaaatcc agcttttgta 2450

tgaggactat agggtgaatt ctctgattag taattttaga tatgtccttt 2500

cctaaaaatg aataaaattt atgaatatga 2530

<210> 296
<211> 413
<212> PRT
<213> Homo sapiens

<400> 296

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Met Glu Asn Met Leu Leu Trp Leu Ile Phe Phe Thr Pro Gly Trp
1               5                   10                  15

Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His
                20                  25                  30

Leu Arg Lys Val Pro Arg Ile Val Ser Glu Arg Thr Phe His Leu
                35                  40                  45

Thr Ser Pro Ala Phe Glu Ala Asp Ala Lys Met Met Val Asn Thr
                50                  55                  60

Val Cys Gly Ile Glu Cys Gln Lys Glu Leu Pro Thr Pro Ser Leu
                65                  70                  75

Ser Glu Leu Glu Asp Tyr Leu Ser Tyr Glu Thr Val Phe Glu Asn
                80                  85                  90

Gly Thr Arg Thr Leu Thr Arg Val Lys Val Gln Asp Leu Val Leu
                95                  100                 105

Glu Pro Thr Gln Asn Ile Thr Thr Lys Gly Val Ser Val Arg Arg
                110                 115                 120

Lys Arg Gln Val Tyr Gly Thr Asp Ser Arg Phe Ser Ile Leu Asp
                125                 130                 135

Lys Arg Phe Leu Thr Asn Phe Pro Phe Ser Thr Ala Val Lys Leu
                140                 145                 150

Ser Thr Gly Cys Ser Gly Ile Leu Ile Ser Pro Gln His Val Leu
                155                 160                 165

Thr Ala Ala His Cys Val His Asp Gly Lys Asp Tyr Val Lys Gly
                170                 175                 180

Ser Lys Lys Leu Arg Val Gly Leu Leu Lys Met Arg Asn Lys Ser
                185                 190                 195

Gly Gly Lys Lys Arg Arg Gly Ser Lys Arg Ser Arg Arg Glu Ala
                200                 205                 210
```

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Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu
                215                 220                 225

Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln
                230                 235                 240

Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys
                245                 250                 255

Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp
                260                 265                 270

Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Arg Ala
                275                 280                 285

His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys
                290                 295                 300

Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp
                305                 310                 315

Arg Ala Asp Gln Leu Val Tyr Arg Phe Cys Ser Val Ser Asp Glu
                320                 325                 330

Ser Asn Asp Leu Leu Tyr Gln Tyr Cys Asp Ala Glu Ser Gly Ser
                335                 340                 345

Thr Gly Ser Gly Val Tyr Leu Arg Leu Lys Asp Pro Asp Lys Lys
                350                 355                 360

Asn Trp Lys Arg Lys Ile Ile Ala Val Tyr Ser Gly His Gln Trp
                365                 370                 375

Val Asp Val His Gly Val Gln Lys Asp Tyr Asn Val Ala Val Arg
                380                 385                 390

Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Leu Trp Ile His Gly
                395                 400                 405

Asn Asp Ala Asn Cys Ala Tyr Gly
                410
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<210> 297
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 297
gcatctgcag gagagagcga aggg 24

<210> 298
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 298
catcgttccc gtgaatccag aggc 24

<210> 299
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 299
gaagggaggc cttcctttca gtggacccgg gtcaagaata cccac 45

<210> 300
<211> 1869
<212> DNA
<213> Homo sapiens

<400> 300
aatgtgagag gggctgatgg aagctgatag gcaggactgg agtgttagca 50

ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100

tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150

gcaactcctg gcacactgct cctctttctg gctttcctgc tcctgagttc 200

caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250

gcccatggag tgaatgctca cgcacctgcg ggggaggggc ctcctactct 300

ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata 350

cagaacatgc agtaatgtgg actgcccacc agaagcaggt gatttccgag 400

ctcagcaatg ctcagctcat aatgatgtca agcaccatgg ccagttttat 450

gaatggcttc ctgtgtctaa tgaccctgac aacccatgtt cactcaagtg 500

ccaagccaaa ggaacaaccc tggttgttga actagcacct aaggtcttag 550

atggtacgcg ttgctataca gaatctttgg atatgtgcat cagtggttta 600

tgccaaattg ttggctgcga tcaccagctg ggaagcaccg tcaaggaaga 650

taactgtggg gtctgcaacg gagatgggtc cacctgccgg ctggtccgag 700

ggcagtataa atcccagctc tccgcaacca aatcggatga tactgtggtt 750

gcacttccct atggaagtag acatattcgc cttgtcttaa aaggtcctga 800

tcacttatat ctggaaacca aaaccctcca ggggactaaa ggtgaaaaca 850

gtctcagctc cacaggaact ttccttgtgg acaattctag tgtggacttc 900 cagaaatttc cagacaaaga gatactgaga atggctggac cactcacagc 950

agatttcatt gtcaagattc gtaactcggg ctccgctgac agtacagtcc 1000

agttcatctt ctatcaaccc atcatccacc gatggaggga gacggatttc 1050

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gtgctacgat ctgaggagca accgtgtggt tgctgaccaa tactgtcact 1150

attacccaga gaacatcaaa cccaaaccca agcttcagga gtgcaacttg 1200

gatccttgtc cagccagtga cggatacaag cagatcatgc cttatgacct 1250

ctaccatccc cttcctcggt gggaggccac cccatggacc gcgtgctcct 1300

cctcgtgtgg gggggcatc cagagccggg cagtttcctg tgtggaggag 1350

gacatccagg ggcatgtcac ttcagtggaa gagtggaaat gcatgtacac 1400

ccctaagatg cccatcgcgc agccctgcaa catttttgac tgccctaaat 1450

ggctggcaca ggagtggtct ccgtgcacag tgacatgtgg ccagggcctc 1500

agataccgtg tggtcctctg catcgaccat cgaggaatgc acacaggagg 1550

ctgtagccca aaaacaaagc cccacataaa agaggaatgc atcgtaccca 1600

ctccctgcta taaacccaaa gagaaacttc cagtcgaggc caagttgcca 1650

tggttcaaac aagctcaaga gctagaagaa ggagctgctg tgtcagagga 1700

gccctcgtaa gttgtaaaag cacagactgt tctatatttg aaactgtttt 1750

gtttaaagaa agcagtgtct cactggttgt agctttcatg ggttctgaac 1800

taagtgtaat catctcacca aagctttttg gctctcaaat taaagattga 1850

ttagtttcaa aaaaaaaaa 1869

<210> 301
<211> 525
<212> PRT
<213> Homo sapiens

<400> 301
Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe
1   5   10   15

Leu Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu
                20   25   30

Asp Arg Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys
                35   40   45

Ser Arg Thr Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys
                50   55   60

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Leu Ser Ser Lys Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr
                 65                  70                  75

Cys Ser Asn Val Asp Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala
                 80                  85                  90

Gln Gln Cys Ser Ala His Asn Asp Val Lys His His Gly Gln Phe
                 95                 100                 105

Tyr Glu Trp Leu Pro Val Ser Asn Asp Pro Asp Asn Pro Cys Ser
                110                 115                 120

Leu Lys Cys Gln Ala Lys Gly Thr Thr Leu Val Val Glu Leu Ala
                125                 130                 135

Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp
                140                 145                 150

Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln
                155                 160                 165

Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly
                170                 175                 180

Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln
                185                 190                 195

Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr
                200                 205                 210

Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu
                215                 220                 225

Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser
                230                 235                 240

Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp
                245                 250                 255

Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro
                260                 265                 270

Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala
                275                 280                 285

Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg
                290                 295                 300

Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly
                305                 310                 315

Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn
                320                 325                 330

Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile
                335                 340                 345

Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro
```

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                    350                 355                 360

Ala Ser Asp Gly Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His
                365                 370                 375

Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser
                380                 385                 390

Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu
                395                 400                 405

Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys
                410                 415                 420

Met Tyr Thr Pro Lys Met Pro Ile Ala Gln Pro Cys Asn Ile Phe
                425                 430                 435

Asp Cys Pro Lys Trp Leu Ala Gln Glu Trp Ser Pro Cys Thr Val
                440                 445                 450

Thr Cys Gly Gln Gly Leu Arg Tyr Arg Val Val Leu Cys Ile Asp
                455                 460                 465

His Arg Gly Met His Thr Gly Gly Cys Ser Pro Lys Thr Lys Pro
                470                 475                 480

His Ile Lys Glu Glu Cys Ile Val Pro Thr Pro Cys Tyr Lys Pro
                485                 490                 495

Lys Glu Lys Leu Pro Val Glu Ala Lys Leu Pro Trp Phe Lys Gln
                500                 505                 510

Ala Gln Glu Leu Glu Glu Gly Ala Ala Val Ser Glu Glu Pro Ser
                515                 520                 525

<210> 302
<211> 1533
<212> DNA
<213> Homo sapiens

<400> 302
 cggacgcgtg ggcggcggct gcggaactcc cgtggagggg ccggtgggcc 50

 ctcgggcctg acagatggca gtggccactg cggcggcagt actggccgct 100

 ctgggcgggg cgctgtggct ggcggcccgc cggttcgtgg ggcccagggt 150

 ccagcggctg cgcagaggcg ggaccccgg cctcatgcac gggaagactg 200

 tgctgatcac cggggcgaac agcggcctgg gccgcgccac ggccgccgag 250

 ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300

 cgccgaggag gcggcgggtc agctccgccg cgagctccgc caggccgcgg 350

 agtgcggccc agagcctggc gtcagcgggg tgggcgagct catagtccgg 400

 gagctggacc tcgcctcgct gcgctcggtg cgcgccttct gccaggaaat 450
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gctccaggaa gagcctaggc tggatgtctt gatcaataac gcagggatct 500

tccagtgccc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550

gtgaaccatc tggggcactt tctactcacc aatcttctcc ttggactcct 600

caaaagttca gctcccagca ggattgtggt agtttcttcc aaactttata 650

aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700

aaaagctttt gttatagccg gagcaaactg gctaacattc tttttaccag 750

ggaactagcc cgccgcttag aaggcacaaa tgtcaccgtc aatgtgttgc 800

atcctggtat tgtacggaca aatctgggga ggcacataca cattccactg 850

ttggtcaaac cactcttcaa tttggtgtca tgggcttttt tcaaaactcc 900

agtagaaggt gcccagactt ccatttattt ggcctcttca cctgaggtag 950

aaggagtgtc aggaagatac tttggggatt gtaaagagga agaactgttg 1000

cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050

agtgatggtt ggcctgctaa aataggaaca aggagtaaaa gagctgttta 1100

taaaactgca tatcagttat atctgtgatc aggaatggtg tggattgaga 1150

acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200

ggtacatgtg ggtattttgg agttactgaa aaattatttt tgggataaga 1250

gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300

aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350

tggatgacat attaatattt gtcagaatta agtgactcaa agtgctatcg 1400

agaggttttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450

ttactacaat gtttggtgtt tgtgtggaaa ttatctgcct ggtgtgtgca 1500

cacaagtctt acttggaata aatttactgg tac 1533

<210> 303
<211> 336
<212> PRT
<213> Homo sapiens

<400> 303
Met Ala Val Ala Thr Ala Ala Ala Val Leu Ala Ala Leu Gly Gly
1   5   10   15

Ala Leu Trp Leu Ala Ala Arg Arg Phe Val Gly Pro Arg Val Gln
                20   25   30

Arg Leu Arg Arg Gly Gly Asp Pro Gly Leu Met His Gly Lys Thr
                35   40   45

Val Leu Ile Thr Gly Ala Asn Ser Gly Leu Gly Arg Ala Thr Ala
50 55 60

Ala Glu Leu Leu Arg Leu Gly Ala Arg Val Ile Met Gly Cys Arg
65 70 75

Asp Arg Ala Arg Ala Glu Glu Ala Ala Gly Gln Leu Arg Arg Glu
80 85 90

Leu Arg Gln Ala Ala Glu Cys Gly Pro Glu Pro Gly Val Ser Gly
95 100 105

Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg
110 115 120

Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg
125 130 135

Leu Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr
140 145 150

Met Lys Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His
155 160 165

Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys
170 175 180

Ser Ser Ala Pro Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr
185 190 195

Lys Tyr Gly Asp Ile Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser
200 205 210

Tyr Asn Lys Ser Phe Cys Tyr Ser Arg Ser Lys Leu Ala Asn Ile
215 220 225

Leu Phe Thr Arg Glu Leu Ala Arg Arg Leu Glu Gly Thr Asn Val
230 235 240

Thr Val Asn Val Leu His Pro Gly Ile Val Arg Thr Asn Leu Gly
245 250 255

Arg His Ile His Ile Pro Leu Leu Val Lys Pro Leu Phe Asn Leu
260 265 270

Val Ser Trp Ala Phe Phe Lys Thr Pro Val Glu Gly Ala Gln Thr
275 280 285

Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu Gly Val Ser Gly
290 295 300

Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu Pro Lys Ala
305 310 315

Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser Glu Val
320 325 330

Met Val Gly Leu Leu Lys

<210> 304
<211> 521
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 20, 34, 62, 87, 221, 229
<223> unknown base

<400> 304
ggggattgta aagaggaagn actgtgccca aagntatgga tgaatctgtt 50

gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100

ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150

gtgatcagga atggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200

tttgatattg gaatagcctg ntaagaggna catgtgggta ttttggagtt 250

actgaaaaat tatttttggg ataagagaat ttcagcaaag atgttttaaa 300

tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350

attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400

gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450

tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500

tggaaattat ctgcctggct t 521

<210> 305
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 305
ccaggaaatg ctccaggaag agcc 24

<210> 306
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 306
gcccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 307
aacgcaggga tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308
<211> 1523
<212> DNA
<213> Homo sapiens

<400> 308
gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50

cggagcccag ccctttccta acccaaccca acctagccca gtcccagccg 100

ccagcgcctg tccctgtcac ggaccccagc gttaccatgc atcctgccgt 150

cttcctatcc ttacccgacc tcagatgctc ccttctgctc ctggtaactt 200

gggtttttac tcctgtaaca actgaaataa caagtcttgc tacagagaat 250

atagatgaaa ttttaaacaa tgctgatgtt gctttagtaa atttttatgc 300

tgactggtgt cgtttcagtc agatgttgca tccaattttt gaggaagctt 350

ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400

agagttgatt gtgatcagca ctctgacata gcccagagat acaggataag 450

caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500

aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550

caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccac 600

tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650

cggacaacta tagagttttt gaacgagtag cgaatatttt gcatgatgac 700

tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750

tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800

tgtacttggg agctatgaca aattttgatg tgacttacaa ttggattcaa 850

gataaatgtg ttcctcttgt ccgagaaata acatttgaaa atggagagga 900

attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950

atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000

agtgaaaaag gtacaataaa ctttttacat gccgattgtg acaaatttag 1050 acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100

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actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250

gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttccag 1300

aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350

gctttaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400

cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450

tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500

aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309
<211> 406
<212> PRT
<213> Homo sapiens

<400> 309
Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser
1 5 10 15

Leu Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu
20 25 30

Ile Thr Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn
35 40 45

Ala Asp Val Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe
50 55 60

Ser Gln Met Leu His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile
65 70 75

Lys Glu Glu Phe Pro Asn Glu Asn Gln Val Val Phe Ala Arg Val
80 85 90

Asp Cys Asp Gln His Ser Asp Ile Ala Gln Arg Tyr Arg Ile Ser
95 100 105

Lys Tyr Pro Thr Leu Lys Leu Phe Arg Asn Gly Met Met Met Lys
110 115 120

Arg Glu Tyr Arg Gly Gln Arg Ser Val Lys Ala Leu Ala Asp Tyr
125 130 135

Ile Arg Gln Gln Lys Ser Asp Pro Ile Gln Glu Ile Arg Asp Leu
140 145 150

Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys Arg Asn Ile Ile Gly
155 160 165

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Tyr Phe Glu Gln Lys Asp Ser Asp Asn Tyr Arg Val Phe Glu Arg
                170                 175                 180

Val Ala Asn Ile Leu His Asp Asp Cys Ala Phe Leu Ser Ala Phe
                185                 190                 195

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile
                200                 205                 210

Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly
                215                 220                 225

Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys
                230                 235                 240

Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu
                245                 250                 255

Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys
                260                 265                 270

Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg
                275                 280                 285

Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp
                290                 295                 300

Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro
                305                 310                 315

Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr
                320                 325                 330

Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys
                335                 340                 345

Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe
                350                 355                 360

His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala
                365                 370                 375

Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu
                380                 385                 390

Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu
                395                 400                 405

Leu
```

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<210> 310
<211> 182
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
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<222> 36, 48
<223> unknown base

<400> 310
attaaggaag aatttccaaa tgaaaatcaa gtagtntttg ccagagtnga 50

ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100

caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150

ggtcagcgat cagtgaaagc attggcagat ta 182

<210> 311
<211> 598
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396
<223> unknown base

<400> 311
agaggcctct ctggaagttg tcccgggtgt tcgccgcngg agcccgggtc 50

gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 100

cggagcccag ccctttccta acccaaccca acctagcccn gtcccagccg 150

ccagcgcctg tccctgtcnc gganccccagc gtnaccatgc atcctgccgt 200

cttcctatcc ttacccgacc tcagatgctc ccttctgctc ctggtaactt 250

gggtttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300

atagatgaaa ttttaaacna tgctgatgtg gctttagtca atttttatgc 350

tgactggtgt cgtttcagtc agatgtggca tccaattttt gaggangctt 400

ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450

agagttgatt gtgatcagca ctctgacata gcccagagat acaggataag 500

caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550

aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 312
tgagaggcct ctctggaagt tg 22

<210> 313
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 313
gtcagcgatc agtgaaagc 19

<210> 314
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 314
ccagaatgaa gtagctcggc 20

<210> 315
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 315
ccgactcaaa atgcattgtc 20

<210> 316
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 316
catttggcag gaattgtcc 19

<210> 317
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 317
ggtgctatag gccaaggg 18

<210> 318
<211> 24
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 318
ctgtatctct gggctatgtc agag 24

<210> 319
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 319
ctacatataa tggcacatgt cagcc 25

<210> 320
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 320
cgtcttccta tccttacccg acctcagatg ctcccttctg ctcctg 46

<210> 321
<211> 1333
<212> DNA
<213> Homo sapiens

<400> 321
gcccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50

cgctgctgct cactgccgcg ctcatcttct tcgccatttg gcacattata 100

gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

taccctgaat ccccttgtac tcccagagta cctcatccac gctttcttct 200

gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250

cccctcttgg catatcatat ttggaggtat atgagtagac cagtgatgag 300

tggcccagga ctctatgacc ctacaaccat catgaatgca gatattctag 350

catattgtca gaaggaagga tggtgcaaat tagcttttta tcttctagca 400

ttttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450

caacacacag aagaattggt ccagttaagt gcatgcaaaa agccaccaaa 500

tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550 tgatcagtta ctttaaaaaa tgactcctta ttttttaaat gtttccacat 600

ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650

taaatggtat tacgtataaa ttaatataaa atgattacct ctggtgttga 700

caggtttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750

gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800

cttgtagggc tcattttggt ttcattgaaa cagtatctaa ttataaatta 850

gctgtagata tcaggtgctt ctgatgaagt gaaaatgtat atctgactag 900

tgggaaactt catgggtttc ctcatctgtc atgtcgatga ttatatatgg 950

atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000

tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050

taaatatact tgctttaatt cttaagcata agtaaacatg atataaaaat 1100

atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaatgtgt 1150

ttttatttgt aagacattac ttattaagaa attggttatt atgcttactg 1200

ttctaatctg gtggtaaagg tattcttaag aatttgcagg tactacagat 1250

tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300

gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322
<211> 144
<212> PRT
<213> Homo sapiens

<400> 322

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 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu
  1               5                  10                  15

 Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala
                 20                  25                  30

 Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys
                 35                  40                  45

 Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala
                 50                  55                  60

 Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu
                 65                  70                  75

 Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met
                 80                  85                  90

 Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr
                 95                 100                 105
```

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp
110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr
125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser
140

<210> 323
<211> 477
<212> DNA
<213> Homo sapiens

<400> 323
attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50

tgtaataccc tgaatcccct tgtactccca gagtacctca tccacgcttt 100

cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150

atatgcccct cttggcatat catatttgga ggtatatgag tagaccagtg 200

atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250

tctagcatat tgtcagaagg aaggatggtg caaattagct ttttatcttc 300

tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350

tagaacaaca cacagaagaa ttggtccagt taagtgcatg caaaaagcca 400

ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450

gaatctgatc agttacttta aaaaatg 477

<210> 324
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 324
tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 325
caggaaacag ctatgaccac ctgcacacct gcaaatccat t 41

<210> 326

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 326
gtgcagcaga gtggcttaca 20

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
actggaccaa ttcttctgtg 20

<210> 328
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
gatattctag catattgtca gaaggaagga tggtgcaaat tagct 45

<210> 329
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 329
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50

tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100

ggacccaact ggggctcccg ccgctgctgc tgctgaccat ggccttggcc 150

ggaggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200

tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250

accctaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300

tcaatttgtc agtttgtgga tgatggaatt gacttaaatc gaactaaatt 350

ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400

atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450

caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500 aactctggtg aggtcattct ggagtgacat gatggactcc gcacagagct 550

tcataacctc ttcatggact ttttatcttc aagccgatga cggaaaaata 600

gttatattcc agtctaagcc agaaatccag tacgcaccac atttggagca 650

ggagcctaca aatttgagag aatcatctct aagcaaaatg tcctatctgc 700

aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750

gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800

aactcttgtc ctctcggtga tggtattgct ttggatttgt tgtgcaactg 850

ttgctacagc tgtggagcag tatgttccct ctgagaagct gagtatctat 900

ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950

ttctcttgtg gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000

ctctacctac aaaagtgaat cttgctcatt ctgaaattta agcatttttc 1050

ttttaaaaga caagtgtaat agacatctaa aattccactc ctcatagagc 1100

ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150

caaataaagt tactcaaatc tgtg 1174

<210> 330
<211> 323
<212> PRT
<213> Homo sapiens

<400> 330
Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly
1 5 10 15

Leu Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser
20 25 30

Gly Thr Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr
35 40 45

Ala Ser Cys His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr
50 55 60

Tyr Pro Lys Glu Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg
65 70 75

Leu Phe Ser Ile Cys Gln Phe Val Asp Asp Gly Ile Asp Leu Asn
80 85 90

Arg Thr Lys Leu Glu Cys Glu Ser Ala Cys Thr Glu Ala Tyr Ser
95 100 105

Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln
110 115 120

Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met
125 130 135

Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe
140 145 150

Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser
155 160 165

Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile Phe
170 175 180

Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu
185 190 195

Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu
200 205 210

Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu Asp Gly
215 220 225

Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp
230 235 240

Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp
245 250 255

Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro
260 265 270

Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu
275 280 285

Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg
290 295 300

Ser Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys
305 310 315

Val Asn Leu Ala His Ser Glu Ile
320

<210> 331
<211> 350
<212> DNA
<213> Homo sapiens

<400> 331
ttgggtgata cggcgtcttg ccaccgggcc tgtcagttga cctacccctt 50

gcacacctac cctaaggaag aggagttgta cgcatgtcag agaggttgca 100

ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaatcga 150

actaaattgg aatgtgaatc tgcatgtaca gaagcatatt cccaatctga 200

tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250 aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300

tttcctctaa ctctggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332
<211> 562
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 47
<223> unknown base

<400> 332
cacactggcc ggatctttta gagtcctttg accttgacca agggtcngga 50

aaacagcaac aagctgagct gctgtgacag agggaacaag atggcggcgc 100

cgaagggagc ctttgggtga ggacccaact ggggctcccg ccgctgctgc 150

tgctgaccat ggccttggcc ggaggttcgg ggaccgcttc ggctgaagca 200

tttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250

gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300

agagaggttg caggctgttt tcaatttgtc agtttgtgga tgatggaatt 350

gacttaaatc gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400

ttcccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450

tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500

atgcacctac tctttcctct aactctggtg aggtcattct ggagtgacat 550

gatggactcc gc 562

<210> 333
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 333
acaagctgag ctgctgtgac ag 22

<210> 334
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 334
tgattctggc aaccaagatg gc 22

<210> 335
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 335
atggccttgg ccggaggttc ggggaccgct tcggctgaag 40

<210> 336
<211> 1885
<212> DNA
<213> Homo sapiens

<400> 336
gcgaggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50

cggccccggag gtggggcgcc gctggggccg gcccgcacgg gcttcatctg 100

agggcgcacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150

gcgacaagct gccggagctg caatgggccg cggctgggga ttcttgtttg 200

gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250

cccccggaga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300

ggatgattgt acctgtgatg ttgaaaccat tgatagattt aataactaca 350

ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400

tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450

gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500

ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550

ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600

tctgagtgag gaaacacaga aggctgttct tcagtggacc aagcatgatg 650

attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700

gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750

accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

agccacagac aattaaaaga cctttaaatc ctttggcttc tggtcaaggg 850

acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900

aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950

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tgcatttgag tgcaagatat cttttacaag agacctggtt agaaaagaaa 1000

tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050

tgaaggagaa ggtccaagaa ggcttaagaa cttgtatttt ctctacttaa 1100

tagaactaag ggctttatcc aaagtgttac cattcttcga gcgcccagat 1150

tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatgtt 1200

acttctggaa atacttcatg aaatcaagtc atttcctttg cattttgatg 1250

agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300

gactttcgac tgcattttag aaatatttca agaattatgg attgtgttgg 1350

ttgttttaaa tgtcgtctgt ggggaaagct tcagactcag ggtttgggca 1400

ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450

agtggaccta gttatgaatt ccatctaacc agacaagaaa tagtatcatt 1500

attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaact 1550

tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600

ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650

atagcaatga cagtcttaag ccaaacattt tatataaagt tgcttttgta 1700

aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750

gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtggt 1800

acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337
<211> 468
<212> PRT
<213> Homo sapiens

<400> 337
Met Gly Arg Gly Trp Gly Phe Leu Phe Gly Leu Leu Gly Ala Val
  1               5                  10                  15

Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr
                 20                  25                  30

Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp
                 35                  40                  45

Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg
                 50                  55                  60

Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg
                 65                  70                  75
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Tyr Tyr Lys Val Asn Leu Lys Arg Pro Cys Pro Phe Trp Asn Asp
                80                  85                  90

Ile Ser Gln Cys Gly Arg Arg Asp Cys Ala Val Lys Pro Cys Gln
                95                  100                 105

Ser Asp Glu Val Pro Asp Gly Ile Lys Ser Ala Ser Tyr Lys Tyr
                110                 115                 120

Ser Glu Glu Ala Asn Asn Leu Ile Glu Glu Cys Glu Gln Ala Glu
                125                 130                 135

Arg Leu Gly Ala Val Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys
                140                 145                 150

Ala Val Leu Gln Trp Thr Lys His Asp Asp Ser Ser Asp Asn Phe
                155                 160                 165

Cys Glu Ala Asp Asp Ile Gln Ser Pro Glu Ala Glu Tyr Val Asp
                170                 175                 180

Leu Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp
                185                 190                 195

Ala Trp Lys Ile Trp Asn Val Ile Tyr Glu Glu Asn Cys Phe Lys
                200                 205                 210

Pro Gln Thr Ile Lys Arg Pro Leu Asn Pro Leu Ala Ser Gly Gln
                215                 220                 225

Gly Thr Ser Glu Glu Asn Thr Phe Tyr Ser Trp Leu Glu Gly Leu
                230                 235                 240

Cys Val Glu Lys Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His
                245                 250                 255

Ala Ser Ile Asn Val His Leu Ser Ala Arg Tyr Leu Leu Gln Glu
                260                 265                 270

Thr Trp Leu Glu Lys Lys Trp Gly His Asn Ile Thr Glu Phe Gln
                275                 280                 285

Gln Arg Phe Asp Gly Ile Leu Thr Glu Gly Glu Gly Pro Arg Arg
                290                 295                 300

Leu Lys Asn Leu Tyr Phe Leu Tyr Leu Ile Glu Leu Arg Ala Leu
                305                 310                 315

Ser Lys Val Leu Pro Phe Phe Glu Arg Pro Asp Phe Gln Leu Phe
                320                 325                 330

Thr Gly Asn Lys Ile Gln Asp Glu Glu Asn Lys Met Leu Leu Leu
                335                 340                 345

Glu Ile Leu His Glu Ile Lys Ser Phe Pro Leu His Phe Asp Glu
                350                 355                 360

Asn Ser Phe Phe Ala Gly Asp Lys Lys Glu Ala His Lys Leu Lys
```

365 370 375

Glu Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg Ile Met Asp
380 385 390

Cys Val Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln Thr
395 400 405

Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu
410 415 420

Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu Phe His Leu
425 430 435

Thr Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly Arg Ile
440 445 450

Ser Thr Ser Val Lys Glu Leu Glu Asn Phe Arg Asn Leu Leu Gln
455 460 465

Asn Ile His

<210> 338
<211> 507
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 101, 263, 376, 397, 426
<223> unknown base

<400> 338
gctggaaata tggatgtcat ctacgagaaa ctgttttaag ccacagacaa 50

ttaaaagacc tttaaatcct ttggcttctg gtcaagggac aagtgaagag 100

nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150

ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200

caagatatct tttacaagag acctggttag aaaagaaatg gggacacaac 250

attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300

tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350

ctttatccaa agtgttacca ttcttngagc gcccagattt tcaactnttt 400

actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaaat 450

acttcatgaa atcaagtcat ttcctttgca ttttgatgag aattcatttt 500

tttgctg 507

<210> 339
<211> 20

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 339
aagctgccgg agctgcaatg 20

<210> 340
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 340
ttgcttctta atcctgagcg c 21

<210> 341
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 341
aaaggaggac tttcgactgc 20

<210> 342
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 342
agagattcat ccactgctcc aagtcg 26

<210> 343
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 343
tgtccagaaa caggcacata tcagc 25

<210> 344
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 344
agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345
<211> 1486
<212> DNA
<213> Homo sapiens

<400> 345
cggacgcgtg ggcggacgcg tgggcggacg cgtgggttgg gagggggcag 50

gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100

ggacttctca tactggacag aaaccgatca ggcatggaac tccccttcgt 150

cactcacctg ttcttgcccc tggtgttcct gacaggtctc tgctccccct 200

ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250

gaatttggat acagtgtctt acaacatgtt gggggtggac agcgatggat 300

gctggtgggc gccccctggg atgggccttc aggcgaccgg agggggacg 350

tttatcgctg ccctgtaggg ggggcccaca atgccccatg tgccaagggc 400

cacttaggtg actaccaact gggaaattca tctcatcctg ctgtgaatat 450

gcacctgggg atgtctctgt tagagacaga tggtgatggg ggattcatgg 500

tgagctaagg agagggtggt ggcagtgtct ctgaaggtcc ataaaagaaa 550

aaagagaagt gtggtaaggg aaaatggtct gtgtggaggg gtcaaggagt 600

taaaaaccct agaaagcaaa aggtaggtaa tgtcagggag tagtcttcat 650

gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700

gtaactattt cccccatccc caggcctgtg cccctctctg gtctcgtgct 750

tgtggcagct ctgtcttcag ttctgggata tgtgcccgtg tggatgcttc 800

attccagcct cagggaagcc tggcacccac tgcccaacgt gagccagagg 850

aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900

gggcaaagcg gtatgatgcc tggcaaaggg cctgcatggc tatcctcatt 950

gctacctaat gtgcttgcaa aagctccatg tttcctaaca gattcagact 1000

cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050

caaggtgggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100

catggtgaaa ctccatctct actaaaaaaa aaaaaataca aaaattagct 1150 gggtgcgcta gtgcatgcct gtaatctcat ctactcggga ggctaagaca 1200

ggagactctc acttcaaccc aggaggtgga ggttgcggtg agccaagatt 1250

gtgcctctgc actctagcgt gggtgacaga gtaagcgaga ctccatctca 1300

aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350

gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400

gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450

agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346
<211> 124
<212> PRT
<213> Homo sapiens

<400> 346

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Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe
  1               5                  10                  15

Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro
                 20                  25                  30

Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val
                 35                  40                  45

Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala
                 50                  55                  60

Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg
                 65                  70                  75

Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His
                 80                  85                  90

Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn
                 95                 100                 105

Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly
                110                 115                 120

Phe Met Val Ser
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<210> 347
<211> 509
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 22
<223> unknown base

<400> 347

cacagttccc caccatcact cntcccattc cttccaactt tatttttagc 50

ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100

ggagagggac agaggccaga ggacttctca tactggacag aaaccgatca 150

ggcatggaac tccccttcgt cactcacctg ttcttgcccc tggtgttcct 200

gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250

tcccagggcc accagaagct gaatttggat acagtgtctt acaacatgtt 300

gggggtggac agcgatggat gctggtgggc gccccctggg atgggccttc 350

aggcgaccgg agggggacg tttatcgctg ccctgtaggg ggggcccaca 400

atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450

tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500

tggtgatgg 509

<210> 348
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 348
agggacagag gccagaggac ttc 23

<210> 349
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 349
caggtgcata ttcacagcag gatg 24

<210> 350
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 350
ggaactcccc ttcgtcactc acctgttctt gcccctggtg ttcct 45

<210> 351
<211> 2056
<212> DNA

<213> Homo sapiens

<400> 351

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aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50

catctgggtt tgggcagaaa ggagggtgct tcggagcccg ccctttctga 100

gcttcctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150

tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200

gctttatttt ggaaagaaac aatgttctag gtcaaactga gtctaccaaa 250

tgcagacttt cacaatggtt ctagaagaaa tctggacaag tcttttcatg 300

tggtttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350

tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400

tcttgatgtg gagcccagtg atcgcgcctg gagaaacagt gtactattct 450

gtcgaatacc aggggagta cgagagcctg tacacgagcc acatctggat 500

ccccagcagc tggtgctcac tcactgaagg tcctgagtgt gatgtcactg 550

atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg 600

ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650

ctcaaccatc cttacccgac ctgggatgga gatcaccaaa gatggcttcc 700

acctggttat tgagctggag gacctggggc cccagtttga gttccttgtg 750

gcctactgga ggagggagcc tggtgccgag gaacatgtca aaatggtgag 800

gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850

actgtgtgaa ggcccagaca ttcgtgaagg ccattgggag gtacagcgcc 900

ttcagccaga cagaatgtgt ggaggtgcaa ggagaggcca ttcccctggt 950

actggccctg tttgcctttg ttggcttcat gctgatcctt gtggtcgtgc 1000

cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctgttgcccc 1050

gtggtggtcc tcccagacac cttgaaaata accaattcac cccagaagtt 1100

aatcagctgc agaagggagg aggtggatgc ctgtgccacg gctgtgatgt 1150

ctcctgagga actcctcagg gcctggatct cataggtttg cggaagggcc 1200

caggtgaagc cgagaacctg gtctgcatga catggaaacc atgaggggac 1250

aagttgtgtt tctgttttcc gccacggaca agggatgaga gaagtaggaa 1300

gagcctgttg tctacaagtc tagaagcaac catcagaggc agggtggttt 1350

gtctaacaga acactgactg aggcttaggg gatgtgacct ctagactggg 1400
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ggctgccact tgctggctga gcaaccctgg gaaaagtgac ttcatccctt 1450

cggtcctaag ttttctcatc tgtaatgggg gaattaccta cacacctgct 1500

aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550

tacacccagc acttgcaagg ctagagggaa actggtgaca ctctacagtc 1600

tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650

gatcaaggac tctacacact gggtggcttg gagagcccac tttcccagaa 1700

taatccttga gagaaaagga atcatgggag caatggtgtt gagttcactt 1750

caagcccaat gccggtgcag aggggaatgg cttagcgagc tctacagtag 1800

gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850

acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900

agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950

gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000

aattcagcaa ataaaaaggg ccaccctggc caaaagcggt aaaaaaaaaa 2050

aaaaaa 2056

<210> 352
<211> 311
<212> PRT
<213> Homo sapiens

<400> 352
Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu
 1               5                  10                  15

Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp
                20                  25                  30

Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
                35                  40                  45

Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro
                50                  55                  60

Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu
                65                  70                  75

Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser
                80                  85                  90

Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala
                95                 100                 105

Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln
               110                 115                 120
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Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser
125 130 135

Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe
140 145 150

His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe
155 160 165

Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val
170 175 180

Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met
185 190 195

Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys
200 205 210

Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu
215 220 225

Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe
230 235 240

Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp
245 250 255

Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val
260 265 270

Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile
275 280 285

Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met
290 295 300

Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
305 310

<210> 353
<211> 864
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 654, 711, 748, 827
<223> unknown base

<400> 353
tcctgctgat gcacatctgg gtttggcaaa aggaggttgc ttcgagccgc 50

cctttctagc ttcctggccg gctctagaac aattcaggct tcgctgcgac 100

tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150

agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200 ccaaatgcag actttcacaa tggttctaga agaaatctgg acaagtcttt 250

tcatgtggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300

gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350

gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400

attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450

tggatcccca gcagctggtg ctcactcact gaaggtcctg agtgtgatgt 500

cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550

cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600

agaaactcaa ccatccttac ccgacctggg atggagatca ccaaagatgg 650

cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700

ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750

gaaccccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800

tgacccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850

ggcgctgggt tgat 864

<210> 354
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 354
aggcttcgct gcgactagac ctc 23

<210> 355
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 355
ccaggtcggg taaggatggt tgag 24

<210> 356
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 356
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357
<211> 1670
<212> DNA
<213> Homo sapiens

<400> 357
cccacgcgtc cgcccacgcg tccgagggac aagagagaag agagactgaa 50

acagggagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100

ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150

agaggcagga gctggaaagg agagagggag gaggaggagg agatgcggga 200

tggagacctg gagttaggtg gcttgggaga gcttaatgaa aagagaacgg 250

agaggaggtg tgggttagga accaagaggt agccctgtgg gcagcagaag 300

gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350

ggaaaagagc agaggaaaga ggaaagacac agagagacgg gagagagaag 400

aagagtgggt ttgaagggcg gatctcagtc cctggctgct ttggcatttg 450

gggaactggg actccctgtg gggaggagag gaaagctgga agtcctggag 500

ggacagggtc ccagaaggag gggacagagg agctgagaga ggggggcagg 550

gcgttgggca ggggtccctc ggaggcctcc tggggatggg ggctgcagct 600

cgtctgagcg cccctcgagc gctggtactc tgggctgcac tgggggcagc 650

agctcacatc ggaccagcac ctgaccccga ggactggtgg agctacaagg 700

ataatctcca gggaaacttc gtgccagggc ctcctttctg gggcctggtg 750

aatgcagcgt ggagtctgtg tgctgtgggg aagcggcaga gccccgtgga 800

tgtggagctg aagagggttc tttatgaccc ctttctgccc ccattaaggc 850

tcagcactgg aggagagaag ctccggggaa ccttgtacaa caccggccga 900

catgtctcct tcctgcctgc accccgacct gtggtcaatg tgtctggagg 950

tcccctcctt tacagccacc gactcagtga actgcggctg ctgtttggag 1000

ctcgcgacgg agccggctcg gaacatcaga tcaaccacca gggcttctct 1050

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acgttgccag tacctctaac ccattcctca gtcgcctcct taaccgcgac 1200

accatcactc gcatctccta caagaatgat gcctactttc ttcaagacct 1250 gagcctggag ctcctgttcc ctgaatcctt cggcttcatc acctatcagg 1300

gctctctcag cacccgccc tgctccgaga ctgtcacctg gatcctcatt 1350

gaccgggccc tcaatatcac ctcccttcag atgcactccc tgagactcct 1400

gagccagaat cctccatctc agatcttcca gagcctcagc ggtaacagcc 1450

ggcccctgca gcccttggcc cacagggcac tgaggggcaa cagggacccc 1500

cggcaccccg agaggcgctg ccgaggcccc aactaccgcc tgcatgtgga 1550

tggtgtcccc catggtcgct gagactcccc ttcgaggatt gcacccgccc 1600

gtcctaagcc tccccacaag gcgaggggag ttacccctaa aacaaagcta 1650

ttaaagggac agaatactta 1670

<210> 358
<211> 328
<212> PRT
<213> Homo sapiens

<400> 358
Met Gly Ala Ala Ala Arg Leu Ser Ala Pro Arg Ala Leu Val Leu
1   5   10   15

Trp Ala Ala Leu Gly Ala Ala Ala His Ile Gly Pro Ala Pro Asp
                20   25   30

Pro Glu Asp Trp Trp Ser Tyr Lys Asp Asn Leu Gln Gly Asn Phe
                35   40   45

Val Pro Gly Pro Pro Phe Trp Gly Leu Val Asn Ala Ala Trp Ser
                50   55   60

Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu
                65   70   75

Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser
                80   85   90

Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg
                95   100   105

His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser
                110   115   120

Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu
                125   130   135

Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn
                140   145   150

His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln
                155   160   165

Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly

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                170                 175                 180

Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn
                185                 190                 195

Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile
                200                 205                 210

Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu
                215                 220                 225

Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser
                230                 235                 240

Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile
                245                 250                 255

Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg
                260                 265                 270

Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser
                275                 280                 285

Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg
                290                 295                 300

Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro
                305                 310                 315

Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg
                320                 325

<210> 359
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 359
 tctgctgagg tgcagctcat tcac 24

<210> 360
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 360
 gaggctctgg aagatctgag atgg 24

<210> 361
<211> 50
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic oligonucleotide probe

<400> 361
gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362
<211> 3038
<212> DNA
<213> Homo sapiens

<400> 362
ggcgcctggt tctgcgcgta ctggctgtac ggagcaggag caagaggtcg 50

ccgccagcct ccgccgccga gcctcgttcg tgtccccgcc cctcgctcct 100

gcagctactg ctcagaaacg ctggggcgcc caccctggca gactaacgaa 150

gcagctccct tcccacccca actgcaggtc taattttgga cgctttgcct 200

gccatttctt ccaggttgag ggagccgcag aggcggaggc tcgcgtattc 250

ctgcagtcag cacccacgtc gcccccggac gctcggtgct caggcccttc 300

gcgagcgggg ctctccgtct gcggtccctt gtgaaggctc tgggcggctg 350

cagaggccgg ccgtccggtt tggctcacct ctcccaggaa acttcacact 400

ggagagccaa aaggagtgga agagcctgtc ttggagattt tcctggggaa 450

atcctgaggt cattcattat gaagtgtacc gcgcgggagt ggctcagagt 500

aaccacagtg ctgttcatgg ctagagcaat tccagccatg gtggttccca 550

atgccacttt attggagaaa cttttggaaa aatacatgga tgaggatggt 600

gagtggtgga tagccaaaca acgagggaaa agggccatca cagacaatga 650

catgcagagt attttggacc ttcataataa attacgaagt caggtgtatc 700

caacagcctc taatatggag tatatgacat gggatgtaga gctggaaaga 750

tctgcagaat cctgggctga aagttgcttg tgggaacatg gacctgcaag 800

cttgcttcca tcaattggac agaatttggg agcacactgg ggaagatata 850

ggcccccgac gtttcatgta caatcgtggt atgatgaagt gaaagacttt 900

agctacccat atgaacatga atgcaaccca tattgtccat tcaggtgttc 950

tggccctgta tgtacacatt atacacaggt cgtgtgggca actagtaaca 1000

gaatcggttg tgccattaat ttgtgtcata acatgaacat ctgggggcag 1050

atatggccca aagctgtcta cctggtgtgc aattactccc caaagggaaa 1100

ctggtggggc catgcccctt acaaacatgg gcggccctgt tctgcttgcc 1150 cacctagttt tggaggggc tgtagagaaa atctgtgcta caaagaaggg 1200

tcagacaggt attatccccc tcgagaagag gaaacaaatg aaatagaacg 1250

acagcagtca caagtccatg acacccatgt ccggacaaga tcagatgata 1300

gtagcagaaa tgaagtcata agcgcacagc aaatgtccca aattgtttct 1350

tgtgaagtaa gattaagaga tcagtgcaaa ggaacaacct gcaataggta 1400

cgaatgtcct gctggctgtt tggatagtaa agctaaagtt attggcagtg 1450

tacattatga aatgcaatcc agcatctgta gagctgcaat tcattatggt 1500

ataatagaca atgatggtgg ctgggtagat atcactagac aaggaagaaa 1550

gcattatttc atcaagtcca atagaaatgg tattcaaaca attggcaaat 1600

atcagtctgc taattccttc acagtctcta aagtaacagt tcaggctgtg 1650

acttgtgaaa caactgtgga acagctctgt ccatttcata agcctgcttc 1700

acattgccca agagtatact gtcctcgtaa ctgtatgcaa gcaaatccac 1750

attatgctcg tgtaattgga actcgagttt attctgatct gtccagtatc 1800

tgcagagcag cagtacatgc tggagtggtt cgaaatcacg gtggttatgt 1850

tgatgtaatg cctgtggaca aaagaaagac ctacattgct tcttttcaga 1900

atggaatctt ctcagaaagt ttacagaatc ctccaggagg aaaggcattc 1950

agagtgtttg ctgttgtgtg aaactgaata cttggaagag gaccataaag 2000

actattccaa atgcaatatt tctgaatttt gtataaaact gtaacattac 2050

tgtacagagt acatcaacta ttttcagccc aaaaaggtgc caaatgcata 2100

taaatcttga taaacaaagt ctataaaata aaacatggga cattagcttt 2150

gggaaaagta atgaaaatat aatggtttta gaaatcctgt gttaaatatt 2200

gctatatttt cttagcagtt atttctacag ttaattacat agtcatgatt 2250

gttctacgtt tcatatatta tatggtgctt tgtatatgcc actaataaaa 2300

tgaatctaaa cattgaatgt gaatggccct cagaaaatca tctagtgcat 2350

ttaaaaataa tcgactctaa aactgaaaga aaccttatca cattttcccc 2400

agttcaatgc tatgccatta ccaactccaa ataatctcaa ataattttcc 2450

acttaataac tgtaaagttt ttttctgtta atttaggcat atagaatatt 2500

aaattctgat attgcacttc ttattttata taaaataatc ctttaatatc 2550

caaatgaatc tgttaaaatg tttgattcct tgggaatggc cttaaaaata 2600

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aatgtaataa agtcagagtg gtggtatgaa aacattccta gtgatcatgt 2650

agtaaatgta gggttaagca tggacagcca gagctttcta tgtactgtta 2700

aaattgaggt cacatatttt cttttgtatc ctggcaaata ctcctgcagg 2750

ccaggaagta taatagcaaa aagttgaaca aagatgaact aatgtattac 2800

attaccattg ccactgattt tttttaaatg gtaaatgacc ttgtatataa 2850

atattgccat atcatggtac ctataatggt gatatatttg tttctatgaa 2900

aaatgtattg tgctttgata ctaaaaatct gtaaaatgtt agttttggta 2950

atttttttc tgctggtgga tttacatatt aaattttttc tgctggtgga 3000

taaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

<210> 363
<211> 500
<212> PRT
<213> Homo sapiens

<400> 363
Met Lys Cys Thr Ala Arg Glu Trp Leu Arg Val Thr Thr Val Leu
1               5                   10                  15

Phe Met Ala Arg Ala Ile Pro Ala Met Val Val Pro Asn Ala Thr
                20                  25                  30

Leu Leu Glu Lys Leu Leu Glu Lys Tyr Met Asp Glu Asp Gly Glu
                35                  40                  45

Trp Trp Ile Ala Lys Gln Arg Gly Lys Arg Ala Ile Thr Asp Asn
                50                  55                  60

Asp Met Gln Ser Ile Leu Asp Leu His Asn Lys Leu Arg Ser Gln
                65                  70                  75

Val Tyr Pro Thr Ala Ser Asn Met Glu Tyr Met Thr Trp Asp Val
                80                  85                  90

Glu Leu Glu Arg Ser Ala Glu Ser Trp Ala Glu Ser Cys Leu Trp
                95                  100                 105

Glu His Gly Pro Ala Ser Leu Leu Pro Ser Ile Gly Gln Asn Leu
                110                 115                 120

Gly Ala His Trp Gly Arg Tyr Arg Pro Pro Thr Phe His Val Gln
                125                 130                 135

Ser Trp Tyr Asp Glu Val Lys Asp Phe Ser Tyr Pro Tyr Glu His
                140                 145                 150

Glu Cys Asn Pro Tyr Cys Pro Phe Arg Cys Ser Gly Pro Val Cys
                155                 160                 165

Thr His Tyr Thr Gln Val Val Trp Ala Thr Ser Asn Arg Ile Gly
```

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                170                 175                 180

Cys Ala Ile Asn Leu Cys His Asn Met Asn Ile Trp Gly Gln Ile
                185                 190                 195

Trp Pro Lys Ala Val Tyr Leu Val Cys Asn Tyr Ser Pro Lys Gly
                200                 205                 210

Asn Trp Trp Gly His Ala Pro Tyr Lys His Gly Arg Pro Cys Ser
                215                 220                 225

Ala Cys Pro Pro Ser Phe Gly Gly Gly Cys Arg Glu Asn Leu Cys
                230                 235                 240

Tyr Lys Glu Gly Ser Asp Arg Tyr Tyr Pro Pro Arg Glu Glu Glu
                245                 250                 255

Thr Asn Glu Ile Glu Arg Gln Gln Ser Gln Val His Asp Thr His
                260                 265                 270

Val Arg Thr Arg Ser Asp Asp Ser Ser Arg Asn Glu Val Ile Ser
                275                 280                 285

Ala Gln Gln Met Ser Gln Ile Val Ser Cys Glu Val Arg Leu Arg
                290                 295                 300

Asp Gln Cys Lys Gly Thr Thr Cys Asn Arg Tyr Glu Cys Pro Ala
                305                 310                 315

Gly Cys Leu Asp Ser Lys Ala Lys Val Ile Gly Ser Val His Tyr
                320                 325                 330

Glu Met Gln Ser Ser Ile Cys Arg Ala Ala Ile His Tyr Gly Ile
                335                 340                 345

Ile Asp Asn Asp Gly Gly Trp Val Asp Ile Thr Arg Gln Gly Arg
                350                 355                 360

Lys His Tyr Phe Ile Lys Ser Asn Arg Asn Gly Ile Gln Thr Ile
                365                 370                 375

Gly Lys Tyr Gln Ser Ala Asn Ser Phe Thr Val Ser Lys Val Thr
                380                 385                 390

Val Gln Ala Val Thr Cys Glu Thr Thr Val Glu Gln Leu Cys Pro
                395                 400                 405

Phe His Lys Pro Ala Ser His Cys Pro Arg Val Tyr Cys Pro Arg
                410                 415                 420

Asn Cys Met Gln Ala Asn Pro His Tyr Ala Arg Val Ile Gly Thr
                425                 430                 435

Arg Val Tyr Ser Asp Leu Ser Ser Ile Cys Arg Ala Ala Val His
                440                 445                 450

Ala Gly Val Val Arg Asn His Gly Gly Tyr Val Asp Val Met Pro
                455                 460                 465
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Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile
470 475 480

Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg
485 490 495

Val Phe Ala Val Val
500

<210> 364
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 364
ggacagaatt tgggagcaca ctgg 24

<210> 365
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 365
ccaagagtat actgtcctcg 20

<210> 366
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 366
agcacagatt ttctctacag ccccc 25

<210> 367
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 367
aaccactcca gcatgtactg ctgc 24

<210> 368
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 368
ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369
<211> 1685
<212> DNA
<213> Homo sapiens

<400> 369
gcggagacaa gcgcagagcg cagcgcacgg ccacagacag ccctgggcat 50

ccaccgacgg cgcagccgga gccagcagag ccggaaggcg cgcccccgggc 100

agagaaagcc gagcagagct gggtggcgtc tccgggccgc cgctccgacg 150

ggccagcgcc ctccccatgt ccctgctccc acgccgcgcc cctccggtca 200

gcatgaggct cctggcggcc gcgctgctcc tgctgctgct ggcgctgtac 250

accgcgcgtg tggacgggtc caaatgcaag tgctcccgga agggacccaa 300

gatccgctac agcgacgtga agaagctgga aatgaagcca aagtacccgc 350

actgcgagga gaagatggtt atcatcacca ccaagagcgt gtccaggtac 400

cgaggtcagg agcactgcct gcaccccaag ctgcagagca ccaagcgctt 450

catcaagtgg tacaacgcct ggaacgagaa gcgcagggtc tacgaagaat 500

agggtgaaaa acctcagaag ggaaaactcc aaaccagttg ggagacttgt 550

gcaaaggact ttgcagatta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600

aaaaaaaaaa aaagcctttc tttctcacag gcataagaca caaattatat 650

attgttatga agcacttttt accaacggtc agtttttaca ttttatagct 700

gcgtgcgaaa ggcttccaga tgggagaccc atctctcttg tgctccagac 750

ttcatcacag gctgcttttt atcaaaaagg ggaaaactca tgcctttcct 800

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ctttataagc gcccgggagg aacaatgagc ttggtggaca catttcattg 900

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ctctctgcat ctgttctctg aggaactcaa gtttggttgc cagaaaaatg 1100

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tcccaacctg aggatttctg aaaggttcac aggttcaata tttaatgctt 1250

cagaagcatg tgaggttccc aacactgtca gcaaaaacct taggagaaaa 1300

cttaaaaata tatgaataca tgcgcaatac acagctacag acacacattc 1350

tgttgacaag ggaaaacctt caaagcatgt ttctttccct caccacaaca 1400

gaacatgcag tactaaagca atatatttgt gattccccat gtaattcttc 1450

aatgttaaac agtgcagtcc tctttcgaaa gctaagatga ccatgcgccc 1500

tttcctctgt acatataccc ttaagaacgc cccctccaca cactgccccc 1550

cagtatatgc cgcattgtac tgctgtgtta tatgctatgt acatgtcaga 1600

aaccattagc attgcatgca ggtttcatat tctttctaag atggaaagta 1650

ataaaatata tttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370
<211> 111
<212> PRT
<213> Homo sapiens

<400> 370
Met Ser Leu Leu Pro Arg Arg Ala Pro Pro Val Ser Met Arg Leu
1   5   10   15

Leu Ala Ala Ala Leu Leu Leu Leu Leu Leu Ala Leu Tyr Thr Ala
                20   25   30

Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys
                35   40   45

Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
                50   55   60

Pro His Cys Glu Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val
                65   70   75

Ser Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln
                80   85   90

Ser Thr Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys
                95   100   105

Arg Arg Val Tyr Glu Glu
                110

<210> 371
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371
cagcgccctc cccatgtccc tg 22

<210> 372
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 372
tcccaactgg tttggagttt tccc 24

<210> 373
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 373
ctccggtcag catgaggctc ctggcggccg ctgctcctgc tgctg 45

<210> 374
<211> 3113
<212> DNA
<213> Homo sapiens

<400> 374
gccccaggga ctgctatggc ttcctttgtt gttcaccccg gtctgcgtca 50

tgttaaactc caatgtcctc ctgtggttaa ctgctcttgc catcaagttc 100

accctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150

caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200

tggagcagta cttaggggtc ccctatgcct caccccccac tggagagagg 250

cggtttcagc cccagaacc cccgtcctcc tggactggca tccgaaatac 300

tactcagttt gctgctgtgt gcccccagca cctggatgag agatccttac 350

tgcatgacat gctgcccatc tggtttaccg ccaatttgga tactttgatg 400

acctatgttc aagatcaaaa tgaagactgc ctttacttaa acatctacgt 450

gcccacggaa gatggagcca acacaaagaa aaacgcagat gatataacga 500

gtaatgaccg tggtgaagac gaagatattc atgatcagaa cagtaagaag 550

cccgtcatgg tctatatcca tgggggatct tacatggagg gcaccggcaa 600

catgattgac ggcagcattt tggcaagcta cggaaacgtc atcgtgatca 650 ccattaacta ccgtctggga atactagggt ttttaagtac cggtgaccag 700

gcagcaaaag gcaactatgg gctcctggat cagattcaag cactgcggtg 750

gattgaggag aatgtgggag cctttggcgg ggaccccaag agagtgacca 800

tctttggctc gggggctggg gcctcctgtg tcagcctgtt gaccctgtcc 850

cactactcag aaggtctctt ccagaaggcc atcattcaga gcggcaccgc 900

cctgtccagc tgggcagtga actaccagcc ggccaagtac actcggatat 950

tggcagacaa ggtcggctgc aacatgctgg acaccacgga catggtagaa 1000

tgcctgcgga acaagaacta caaggagctc atccagcaga ccatcacccc 1050

ggccacctac cacatagcct tcgggccggt gatcgacggc gacgtcatcc 1100

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aaccaccaaa cgcccagcaa tcactcctgc caacaatccc aaacactcta 2000

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acaagaggcg ccatgagact cacaggcgcc ccagtcccca gagaaacacc 2200

acaaatgata tcgctcacat ccagaacgaa gagatcatgt ctctgcagat 2250

gaagcagctg gaacacgatc acgagtgtga gtcgctgcag gcacacgaca 2300

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gacaaaacag tacaaattta ccccacggac attccaccac tagagtatag 2500

ctttgcccta tttcccttcc tatccctctg ccctacccgc tcagcaacat 2550

agaagaggga aggaaagaga gaaggaaaga gagagagaaa gaaagtctcc 2600

agaccaggaa tgtttttgtc ccactgactt aagacaaaaa tgcaaaaagg 2650

cagtcatccc atcccggcag acccttatcg ttggtgtttt ccagtattac 2700

aagatcaact tctgaccctg tgaaatgtga gaagtacaca tttctgttaa 2750

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gacatcacca tttcaaggcc ccgggtgttt ccaacgtcat ggaagcagct 2850

gacacttctg aaactcagcc aaggacactt gatatttttt aattacaatg 2900

gaagtttaaa catttctttc tgtgccacac aatggatggc tctccttaag 2950

tgaagaaaga gtcaatgaga ttttgcccag cacatggagc tgtaatccag 3000

agagaaggaa acgtagaaat ttattattaa aagaatggac tgtgcagcga 3050

aatctgtacg gttctgtgca aagaggtgtt ttgccagcct gaactatatt 3100

taagagactt tgt 3113

<210> 375
<211> 816
<212> PRT
<213> Homo sapiens

<400> 375

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Met Leu Asn Ser Asn Val Leu Leu Trp Leu Thr Ala Leu Ala Ile
  1               5                  10                  15

Lys Phe Thr Leu Ile Asp Ser Gln Ala Gln Tyr Pro Val Val Asn
                 20                  25                  30

Thr Asn Tyr Gly Lys Ile Arg Gly Leu Arg Thr Pro Leu Pro Asn
                 35                  40                  45

Glu Ile Leu Gly Pro Val Glu Gln Tyr Leu Gly Val Pro Tyr Ala
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50 55 60

Ser Pro Pro Thr Gly Glu Arg Arg Phe Gln Pro Pro Glu Pro Pro
65 70 75

Ser Ser Trp Thr Gly Ile Arg Asn Thr Thr Gln Phe Ala Ala Val
80 85 90

Cys Pro Gln His Leu Asp Glu Arg Ser Leu Leu His Asp Met Leu
95 100 105

Pro Ile Trp Phe Thr Ala Asn Leu Asp Thr Leu Met Thr Tyr Val
110 115 120

Gln Asp Gln Asn Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Val Pro
125 130 135

Thr Glu Asp Gly Ala Asn Thr Lys Lys Asn Ala Asp Asp Ile Thr
140 145 150

Ser Asn Asp Arg Gly Glu Asp Glu Asp Ile His Asp Gln Asn Ser
155 160 165

Lys Lys Pro Val Met Val Tyr Ile His Gly Gly Ser Tyr Met Glu
170 175 180

Gly Thr Gly Asn Met Ile Asp Gly Ser Ile Leu Ala Ser Tyr Gly
185 190 195

Asn Val Ile Val Ile Thr Ile Asn Tyr Arg Leu Gly Ile Leu Gly
200 205 210

Phe Leu Ser Thr Gly Asp Gln Ala Ala Lys Gly Asn Tyr Gly Leu
215 220 225

Leu Asp Gln Ile Gln Ala Leu Arg Trp Ile Glu Glu Asn Val Gly
230 235 240

Ala Phe Gly Gly Asp Pro Lys Arg Val Thr Ile Phe Gly Ser Gly
245 250 255

Ala Gly Ala Ser Cys Val Ser Leu Leu Thr Leu Ser His Tyr Ser
260 265 270

Glu Gly Leu Phe Gln Lys Ala Ile Ile Gln Ser Gly Thr Ala Leu
275 280 285

Ser Ser Trp Ala Val Asn Tyr Gln Pro Ala Lys Tyr Thr Arg Ile
290 295 300

Leu Ala Asp Lys Val Gly Cys Asn Met Leu Asp Thr Thr Asp Met
305 310 315

Val Glu Cys Leu Arg Asn Lys Asn Tyr Lys Glu Leu Ile Gln Gln
320 325 330

Thr Ile Thr Pro Ala Thr Tyr His Ile Ala Phe Gly Pro Val Ile
335 340 345

Asp Gly Asp Val Ile Pro Asp Asp Pro Gln Ile Leu Met Glu Gln
350 355 360

Gly Glu Phe Leu Asn Tyr Asp Ile Met Leu Gly Val Asn Gln Gly
365 370 375

Glu Gly Leu Lys Phe Val Asp Gly Ile Val Asp Asn Glu Asp Gly
380 385 390

Val Thr Pro Asn Asp Phe Asp Phe Ser Val Ser Asn Phe Val Asp
395 400 405

Asn Leu Tyr Gly Tyr Pro Glu Gly Lys Asp Thr Leu Arg Glu Thr
410 415 420

Ile Lys Phe Met Tyr Thr Asp Trp Ala Asp Lys Glu Asn Pro Glu
425 430 435

Thr Arg Arg Lys Thr Leu Val Ala Leu Phe Thr Asp His Gln Trp
440 445 450

Val Ala Pro Ala Val Ala Ala Asp Leu His Ala Gln Tyr Gly Ser
455 460 465

Pro Thr Tyr Phe Tyr Ala Phe Tyr His His Cys Gln Ser Glu Met
470 475 480

Lys Pro Ser Trp Ala Asp Ser Ala His Gly Asp Glu Val Pro Tyr
485 490 495

Val Phe Gly Ile Pro Met Ile Gly Pro Thr Glu Leu Phe Ser Cys
500 505 510

Asn Phe Ser Lys Asn Asp Val Met Leu Ser Ala Val Val Met Thr
515 520 525

Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp Pro Asn Gln Pro Val
530 535 540

Pro Gln Asp Thr Lys Phe Ile His Thr Lys Pro Asn Arg Phe Glu
545 550 555

Glu Val Ala Trp Ser Lys Tyr Asn Pro Lys Asp Gln Leu Tyr Leu
560 565 570

His Ile Gly Leu Lys Pro Arg Val Arg Asp His Tyr Arg Ala Thr
575 580 585

Lys Val Ala Phe Trp Leu Glu Leu Val Pro His Leu His Asn Leu
590 595 600

Asn Glu Ile Phe Gln Tyr Val Ser Thr Thr Thr Lys Val Pro Pro
605 610 615

Pro Asp Met Thr Ser Phe Pro Tyr Gly Thr Arg Arg Ser Pro Ala
620 625 630

Lys Ile Trp Pro Thr Thr Lys Arg Pro Ala Ile Thr Pro Ala Asn

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                635                 640                 645

Asn Pro Lys His Ser Lys Asp Pro His Lys Thr Gly Pro Glu Asp
                650                 655                 660

Thr Thr Val Leu Ile Glu Thr Lys Arg Asp Tyr Ser Thr Glu Leu
                665                 670                 675

Ser Val Thr Ile Ala Val Gly Ala Ser Leu Leu Phe Leu Asn Ile
                680                 685                 690

Leu Ala Phe Ala Ala Leu Tyr Tyr Lys Lys Asp Lys Arg Arg His
                695                 700                 705

Glu Thr His Arg Arg Pro Ser Pro Gln Arg Asn Thr Thr Asn Asp
                710                 715                 720

Ile Ala His Ile Gln Asn Glu Glu Ile Met Ser Leu Gln Met Lys
                725                 730                 735

Gln Leu Glu His Asp His Glu Cys Glu Ser Leu Gln Ala His Asp
                740                 745                 750

Thr Leu Arg Leu Thr Cys Pro Pro Asp Tyr Thr Leu Thr Leu Arg
                755                 760                 765

Arg Ser Pro Asp Asp Ile Pro Leu Met Thr Pro Asn Thr Ile Thr
                770                 775                 780

Met Ile Pro Asn Thr Leu Thr Gly Met Gln Pro Leu His Thr Phe
                785                 790                 795

Asn Thr Phe Ser Gly Gly Gln Asn Ser Thr Asn Leu Pro His Gly
                800                 805                 810

His Ser Thr Thr Arg Val
                815
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<210> 376
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 376
ggcaagctac ggaaacgtca tcgtg 25

<210> 377
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 377

aaccccgag ccaaaagatg gtcac 25

<210> 378
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 378
gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379
<211> 2461
<212> DNA
<213> Homo sapiens

<400> 379
gggaaagatg gcggcgactc tgggacccct tgggtcgtgg cagcagtggc 50

ggcgatgttt gtcggctcgg gatgggtcca ggatgttact ccttcttctt 100

ttgttggggt ctgggcaggg gccacagcaa gtcggggcgg gtcaaacgtt 150

cgagtacttg aaacgggagc actcgctgtc gaagccctac cagggtgtgg 200

gcacaggcag ttcctcactg tggaatctga tgggcaatgc catggtgatg 250

acccagtata tccgccttac cccagatatg caaagtaaac agggtgcctt 300

gtggaaccgg gtgccatgtt tcctgagaga ctgggagttg caggtgcact 350

tcaaaatcca tggacaagga aagaagaatc tgcatgggga tggcttggca 400

atctggtaca caaaggatcg gatgcagcca gggcctgtgt ttggaaacat 450

ggacaaattt gtggggctgg gagtatttgt agacacctac cccaatgagg 500

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gaggaaaagc tccatcgaga tgtgttcttg ccctcagtgg acaatatgaa 900

gctgcctgag atgacagctc cactgccgcc cctgagtggc ctggccctct 950

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aagccaccca ccccagggca atgctgctgt gatgtgcctt tccctgcagt 1300

ccttccatgt gggagcagag gtgtgaagag aatttacgtg gttgtgatgc 1350

caaaatcaca gaacagaatt tcatagccca ggctgccgtg ttgtttgact 1400

cagaaggccc ttctacttca gttttgaatc cacaaagaat taaaaactgg 1450

taacaccaca ggctttctga ccatccattc gttgggtttt gcatttgacc 1500

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tcttccctgc cttaccttcc tttcactcca ttcattgtcc tctctgtgtg 1600

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catctgtgcc tggaagagtt cactgtcatt gagcagcaca gcctgagtgc 2200

tggcctctgt caacccttat tccactgcct tatttgacaa ggggttacat 2250

gctgctcacc ttactgccct gggattaaat cagttacagg ccagagtctc 2300

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<210> 380
<211> 348
<212> PRT
<213> Homo sapiens

<400> 380
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Arg Cys Leu Ser Ala Arg Asp Gly Ser Arg Met Leu Leu Leu Leu
                20   25   30

Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln Val Gly Ala Gly
                35   40   45

Gln Thr Phe Glu Tyr Leu Lys Arg Glu His Ser Leu Ser Lys Pro
                50   55   60

Tyr Gln Gly Val Gly Thr Gly Ser Ser Ser Leu Trp Asn Leu Met
                65   70   75

Gly Asn Ala Met Val Met Thr Gln Tyr Ile Arg Leu Thr Pro Asp
                80   85   90

Met Gln Ser Lys Gln Gly Ala Leu Trp Asn Arg Val Pro Cys Phe
                95   100   105

Leu Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln
                110   115   120

Gly Lys Lys Asn Leu His Gly Asp Gly Leu Ala Ile Trp Tyr Thr
                125   130   135

Lys Asp Arg Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys
                140   145   150

Phe Val Gly Leu Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu
                155   160   165

Lys Gln Gln Glu Arg Val Phe Pro Tyr Ile Ser Ala Met Val Asn
                170   175   180

Asn Gly Ser Leu Ser Tyr Asp His Glu Arg Asp Gly Arg Pro Thr
                185   190   195

Glu Leu Gly Gly Cys Thr Ala Ile Val Arg Asn Leu His Tyr Asp
                200   205   210

Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu Thr Ile Met
                215   220   225

Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile Glu Val
                230   235   240

Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser Ser
                245   250   255

Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys
260 265 270

Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu
275 280 285

His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro
290 295 300

Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe
305 310 315

Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val
320 325 330

Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys
335 340 345

Arg Phe Tyr

<210> 381
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 381
cettgggtcg tggcagcagt gg 22

<210> 382
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 382
cactctccag gctgcatgct cagg 24

<210> 383
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 383
gtcaaacgtt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<210> 384
<211> 3150
<212> DNA
<213> Homo sapiens

<400> 384

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gggacatgtt tgtagccctg ggtggcagtg gtacaaatta ttatgatgca 1700

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ccacagatgg ttggggttga acagtaagca cattgctgca atgtggtacg 1900

tgaattgctt ggtacaaaat ggccagttca cagaggaata gaaggtactt 1950

tatcatagcc agacttcgct tagaatgcca gaataatata gttcaagacc 2000

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tgtgatggaa ccagcacacc tcaaccaaaa ttttttttaat cttagacatt 2100

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<210> 385
<211> 480
<212> PRT
<213> Homo sapiens

<400> 385
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Leu Leu Ala Phe Val Ser Leu Ser Leu Gln Phe Phe His Leu Ile
20   25   30

Pro Val Ser Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys
35   40   45

Arg Ile Met Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro
50   55   60

Val Tyr Glu Ala Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu
65   70   75

Arg Ser Met Glu Gly His Ala Pro His His Phe Lys Leu Val Ser
80   85   90

Val His Val Phe Ile Arg His Gly Asp Arg Tyr Pro Leu Tyr Val
95   100   105

Ile Pro Lys Thr Lys Arg Pro Glu Ile Asp Cys Thr Leu Val Ala
110   115   120

Asn Arg Lys Pro Tyr His Pro Lys Leu Glu Ala Phe Ile Ser His
125   130   135

Met Ser Lys Gly Ser Gly Ala Ser Phe Glu Ser Pro Leu Asn Ser
140   145   150

Leu Pro Leu Tyr Pro Asn His Pro Leu Cys Glu Met Gly Glu Leu
155   160   165

Thr Gln Thr Gly Val Val Gln His Leu Gln Asn Gly Gln Leu Leu
170   175   180

Arg Asp Ile Tyr Leu Lys Lys His Lys Leu Leu Pro Asn Asp Trp
185   190   195

Ser Ala Asp Gln Leu Tyr Leu Glu Thr Thr Gly Lys Ser Arg Thr
200   205   210

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Leu Gln Ser Gly Leu Ala Leu Leu Tyr Gly Phe Leu Pro Asp Phe
                215                 220                 225

Asp Trp Lys Lys Ile Tyr Phe Arg His Gln Pro Ser Ala Leu Phe
                230                 235                 240

Cys Ser Gly Ser Cys Tyr Cys Pro Val Arg Asn Gln Tyr Leu Glu
                245                 250                 255

Lys Glu Gln Arg Arg Gln Tyr Leu Leu Arg Leu Lys Asn Ser Gln
                260                 265                 270

Leu Glu Lys Thr Tyr Gly Glu Met Ala Lys Ile Val Asp Val Pro
                275                 280                 285

Thr Lys Gln Leu Arg Ala Ala Asn Pro Ile Asp Ser Met Leu Cys
                290                 295                 300

His Phe Cys His Asn Val Ser Phe Pro Cys Thr Arg Asn Gly Cys
                305                 310                 315

Val Asp Met Glu His Phe Lys Val Ile Lys Thr His Gln Ile Glu
                320                 325                 330

Asp Glu Arg Glu Arg Arg Glu Lys Lys Leu Tyr Phe Gly Tyr Ser
                335                 340                 345

Leu Leu Gly Ala His Pro Ile Leu Asn Gln Thr Ile Gly Arg Met
                350                 355                 360

Gln Arg Ala Thr Glu Gly Arg Lys Glu Glu Leu Phe Ala Leu Tyr
                365                 370                 375

Ser Ala His Asp Val Thr Leu Ser Pro Val Leu Ser Ala Leu Gly
                380                 385                 390

Leu Ser Glu Ala Arg Phe Pro Arg Phe Ala Ala Arg Leu Ile Phe
                395                 400                 405

Glu Leu Trp Gln Asp Arg Glu Lys Pro Ser Glu His Ser Val Arg
                410                 415                 420

Ile Leu Tyr Asn Gly Val Asp Val Thr Phe His Thr Ser Phe Cys
                425                 430                 435

Gln Asp His His Lys Arg Ser Pro Lys Pro Met Cys Pro Leu Glu
                440                 445                 450

Asn Leu Val Arg Phe Val Lys Arg Asp Met Phe Val Ala Leu Gly
                455                 460                 465

Gly Ser Gly Thr Asn Tyr Tyr Asp Ala Cys His Arg Glu Gly Phe
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<210> 386
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 386
ccaagcagct tagagctcca gacc 24

<210> 387
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<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 387
ttccctatgc tctgtattgg catgg 25

<210> 388
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 388
gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

<210> 389
<211> 3313
<212> DNA
<213> Homo sapiens

<400> 389
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cccttttgaa gaacagtact gtggagctat ttaagagata aaaacgaaat 100

atcctttctg ggagttcaag attgtgcagt aattggttag gactctgagc 150

gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200

cacgcgcctg aagcacaaag cagatagcta ggaatgaacc atccctggga 250

gtatgtggaa acaacggagg agctctgact tcccaactgt cccattctat 300

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acttgggagg ctgagtcagg agaattgctt taacctggga ggtggaggtt 3250

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aaactctatc tca 3313

<210> 390
<211> 916
<212> PRT
<213> Homo sapiens

<400> 390

Met Ile Pro Ala Arg Leu His Arg Asp Tyr Lys Gly Leu Val Leu
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Leu Gly Ile Leu Leu Gly Thr Leu Trp Glu Thr Gly Cys Thr Gln
                20   25   30

Ile Arg Tyr Ser Val Pro Glu Glu Leu Glu Lys Gly Ser Arg Val
                35   40   45

Gly Asp Ile Ser Arg Asp Leu Gly Leu Glu Pro Arg Glu Leu Ala
                50   55   60

Glu Arg Gly Val Arg Ile Ile Pro Arg Gly Arg Thr Gln Leu Phe
                65   70   75

Ala Leu Asn Pro Arg Ser Gly Ser Leu Val Thr Ala Gly Arg Ile
                80   85   90

Asp Arg Glu Glu Leu Cys Met Gly Ala Ile Lys Cys Gln Leu Asn
                95   100   105

Leu Asp Ile Leu Met Glu Asp Lys Val Lys Ile Tyr Gly Val Glu
                110   115   120

Val Glu Val Arg Asp Ile Asn Asp Asn Ala Pro Tyr Phe Arg Glu
                125   130   135

Ser Glu Leu Glu Ile Lys Ile Ser Glu Asn Ala Ala Thr Glu Met
                140   145   150

Arg Phe Pro Leu Pro His Ala Trp Asp Pro Asp Ile Gly Lys Asn
                155   160   165

Ser Leu Gln Ser Tyr Glu Leu Ser Pro Asn Thr His Phe Ser Leu
                170   175   180

Ile Val Gln Asn Gly Ala Asp Gly Ser Lys Tyr Pro Glu Leu Val
                185   190   195

Leu Lys Arg Ala Leu Asp Arg Glu Glu Lys Ala Ala His His Leu
                200   205   210

Val Leu Thr Ala Ser Asp Gly Gly Asp Pro Val Arg Thr Gly Thr
                215   220   225

Ala Arg Ile Arg Val Met Val Leu Asp Ala Asn Asp Asn Ala Pro
                230   235   240

Ala Phe Ala Gln Pro Glu Tyr Arg Ala Ser Val Pro Glu Asn Leu
                245   250   255

Ala Leu Gly Thr Gln Leu Leu Val Val Asn Ala Thr Asp Pro Asp
                260   265   270

Glu Gly Val Asn Ala Glu Val Arg Tyr Ser Phe Arg Tyr Val Asp
                275   280   285

Asp Lys Ala Ala Gln Val Phe Lys Leu Asp Cys Asn Ser Gly Thr

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                290                 295                 300

Ile Ser Thr Ile Gly Glu Leu Asp His Glu Glu Ser Gly Phe Tyr
                305                 310                 315

Gln Met Glu Val Gln Ala Met Asp Asn Ala Gly Tyr Ser Ala Arg
                320                 325                 330

Ala Lys Val Leu Ile Thr Val Leu Asp Val Asn Asp Asn Ala Pro
                335                 340                 345

Glu Val Val Leu Thr Ser Leu Ala Ser Ser Val Pro Glu Asn Ser
                350                 355                 360

Pro Arg Gly Thr Leu Ile Ala Leu Leu Asn Val Asn Asp Gln Asp
                365                 370                 375

Ser Glu Glu Asn Gly Gln Val Ile Cys Phe Ile Gln Gly Asn Leu
                380                 385                 390

Pro Phe Lys Leu Glu Lys Ser Tyr Gly Asn Tyr Tyr Ser Leu Val
                395                 400                 405

Thr Asp Ile Val Leu Asp Arg Glu Gln Val Pro Ser Tyr Asn Ile
                410                 415                 420

Thr Val Thr Ala Thr Asp Arg Gly Thr Pro Pro Leu Ser Thr Glu
                425                 430                 435

Thr His Ile Ser Leu Asn Val Ala Asp Thr Asn Asp Asn Pro Pro
                440                 445                 450

Val Phe Pro Gln Ala Ser Tyr Ser Ala Tyr Ile Pro Glu Asn Asn
                455                 460                 465

Pro Arg Gly Val Ser Leu Val Ser Val Thr Ala His Asp Pro Asp
                470                 475                 480

Cys Glu Glu Asn Ala Gln Ile Thr Tyr Ser Leu Ala Glu Asn Thr
                485                 490                 495

Ile Gln Gly Ala Ser Leu Ser Ser Tyr Val Ser Ile Asn Ser Asp
                500                 505                 510

Thr Gly Val Leu Tyr Ala Leu Ser Ser Phe Asp Tyr Glu Gln Phe
                515                 520                 525

Arg Asp Leu Gln Val Lys Val Met Ala Arg Asp Asn Gly His Pro
                530                 535                 540

Pro Leu Ser Ser Asn Val Ser Leu Ser Leu Phe Val Leu Asp Gln
                545                 550                 555

Asn Asp Asn Ala Pro Glu Ile Leu Tyr Pro Ala Leu Pro Thr Asp
                560                 565                 570

Gly Ser Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Pro Gly
                575                 580                 585
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Tyr Leu Val Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln
590 595 600

Asn Ala Trp Leu Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly
605 610 615

Leu Phe Ser Val Gly Leu His Thr Gly Glu Val Arg Thr Ala Arg
620 625 630

Ala Leu Leu Asp Arg Asp Ala Leu Lys Gln Ser Leu Val Val Ala
635 640 645

Val Gln Asp His Gly Gln Pro Pro Leu Ser Ala Thr Val Thr Leu
650 655 660

Thr Val Ala Val Ala Asp Ser Ile Pro Gln Val Leu Ala Asp Leu
665 670 675

Gly Ser Leu Glu Ser Pro Ala Asn Ser Glu Thr Ser Asp Leu Thr
680 685 690

Leu Tyr Leu Val Val Ala Val Ala Ala Val Ser Cys Val Phe Leu
695 700 705

Ala Phe Val Ile Leu Leu Leu Ala Leu Arg Leu Arg Arg Trp His
710 715 720

Lys Ser Arg Leu Leu Gln Ala Ser Gly Gly Gly Leu Thr Gly Ala
725 730 735

Pro Ala Ser His Phe Val Gly Val Asp Gly Val Gln Ala Phe Leu
740 745 750

Gln Thr Tyr Ser His Glu Val Ser Leu Thr Thr Asp Ser Arg Lys
755 760 765

Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Val
770 775 780

Ser Gln Glu Ser Phe Glu Lys Ser Glu Pro Leu Leu Leu Ser Gly
785 790 795

Asp Ser Val Phe Ser Lys Asp Ser His Gly Leu Ile Glu Val Ser
800 805 810

Leu Tyr Gln Ile Phe Phe Leu Phe Phe Phe Asn Cys Ser Val Ser
815 820 825

Gln Ala Gly Val Gln Arg Tyr Asp His Ser Ser Leu Arg Pro Gln
830 835 840

Thr Pro Arg Leu Lys Gln Leu Ser His Leu Cys Leu Arg Cys Asn
845 850 855

Arg Asp Tyr Arg Cys Lys Pro Pro Thr Val Cys Leu Ser Ile Tyr
860 865 870

Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Leu Leu

                875   880   885

Ser Cys Thr Asp Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp
                890   895   900

Glu Ala Glu Ala Gly Gly Ser Pro Glu Val Gly Ser Leu Arg Pro
                905   910   915

Ala

<210> 391
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 391
tccgtctctg tgaaccgccc cac 23

<210> 392
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 392
ctcgggcgca ttgtcgttct ggtc 24

<210> 393
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 393
ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394
<211> 999
<212> DNA
<213> Homo sapiens

<400> 394
cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50

cccagttaaa aggctccaga atcgtgtacc aggcagagaa ctgaagtact 100

ggggcctcct ccactgggtc cgaatcagta ggtgaccccg cccctggatt 150

ctggaagacc tcaccatggg acgcccccga cctcgtgcgg ccaagacgtg 200

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gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250

aggaggacaa ggtgctgggg ggtcatgagt gccaacccca ttcgcagcct 300

tggcaggcgg ccttgttcca gggccagcaa ctactctgtg gcggtgtcct 350

tgtaggtggc aactgggtcc ttacagctgc ccactgtaaa aaaccgaaat 400

acacagtacg cctgggagac cacagcctac agaataaaga tggcccagag 450

caagaaatac ctgtggttca gtccatccca cacccctgct acaacagcag 500

cgatgtggag gaccacaacc atgatctgat gcttcttcaa ctgcgtgacc 550

aggcatccct ggggtccaaa gtgaagccca tcagcctggc agatcattgc 600

acccagcctg gccagaagtg caccgtctca ggctggggca ctgtcaccag 650

tccccgagag aattttcctg acactctcaa ctgtgcagaa gtaaaaatct 700

ttccccagaa gaagtgtgag gatgcttacc cggggcagat cacagatggc 750

atggtctgtg caggcagcag caaaggggct gacacgtgcc agggcgattc 800

tggaggcccc ctggtgtgtg atggtgcact ccagggcatc acatcctggg 850

gctcagaccc ctgtgggagg tccgacaaac ctggcgtcta taccaacatc 900

tgccgctacc tggactggat caagaagatc ataggcagca agggctgatt 950

ctaggataag cactagatct cccttaataa actcacaact ctctggttc 999
```

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<210> 395
<211> 260
<212> PRT
<213> Homo sapiens

<400> 395
Met Gly Arg Pro Arg Pro Arg Ala Ala Lys Thr Trp Met Phe Leu
 1               5                  10                  15

Leu Leu Leu Gly Gly Ala Trp Ala Gly His Ser Arg Ala Gln Glu
                20                  25                  30

Asp Lys Val Leu Gly Gly His Glu Cys Gln Pro His Ser Gln Pro
                35                  40                  45

Trp Gln Ala Ala Leu Phe Gln Gly Gln Gln Leu Leu Cys Gly Gly
                50                  55                  60

Val Leu Val Gly Gly Asn Trp Val Leu Thr Ala Ala His Cys Lys
                65                  70                  75

Lys Pro Lys Tyr Thr Val Arg Leu Gly Asp His Ser Leu Gln Asn
                80                  85                  90

Lys Asp Gly Pro Glu Gln Glu Ile Pro Val Val Gln Ser Ile Pro
                95                 100                 105
```

```
His Pro Cys Tyr Asn Ser Ser Asp Val Glu Asp His Asn His Asp
                110                 115                 120

Leu Met Leu Leu Gln Leu Arg Asp Gln Ala Ser Leu Gly Ser Lys
                125                 130                 135

Val Lys Pro Ile Ser Leu Ala Asp His Cys Thr Gln Pro Gly Gln
                140                 145                 150

Lys Cys Thr Val Ser Gly Trp Gly Thr Val Thr Ser Pro Arg Glu
                155                 160                 165

Asn Phe Pro Asp Thr Leu Asn Cys Ala Glu Val Lys Ile Phe Pro
                170                 175                 180

Gln Lys Lys Cys Glu Asp Ala Tyr Pro Gly Gln Ile Thr Asp Gly
                185                 190                 195

Met Val Cys Ala Gly Ser Ser Lys Gly Ala Asp Thr Cys Gln Gly
                200                 205                 210

Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Ala Leu Gln Gly Ile
                215                 220                 225

Thr Ser Trp Gly Ser Asp Pro Cys Gly Arg Ser Asp Lys Pro Gly
                230                 235                 240

Val Tyr Thr Asn Ile Cys Arg Tyr Leu Asp Trp Ile Lys Lys Ile
                245                 250                 255

Ile Gly Ser Lys Gly
                260
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<210> 396
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 396
cagcctacag aataaagatg gccc 24

<210> 397
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 397
ggtgcaatga tctgccaggc tgat 24

<210> 398
<211> 48
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 398
agaaatacct gtggttcagt ccatcccaaa cccctgctac aacagcag 48

<210> 399
<211> 2236
<212> DNA
<213> Homo sapiens

<400> 399
ggcgccggtg caccgggcgg gctgagcgcc tcctgcggcc cggcctgcgc 50

gccccggccc gccgcgccgc ccacgcccca accccggccc gcgcccccta 100

gccccccgccc gggcccgcgc ccgcgcccgc gcccaggtga gcgctccgcc 150

cgccgcgagg ccccgccccg gcccgccccc gccccgcccc ggccggcggg 200

ggaaccgggc ggattcctcg cgcgtcaaac cacctgatcc cataaaacat 250

tcatcctccc ggcggcccgc gctgcgagcg ccccgccagt ccgcgccgcc 300

gccgccctcg ccctgtgcgc cctgcgcgcc ctgcgcaccc gcggcccgag 350

cccagccaga gccgggcgga gcggagcgcg ccgagcctcg tcccgcggcc 400

gggccggggc cgggccgtag cggcggcgcc tggatgcgga cccggccgcg 450

gggagacggg cgcccgcccc gaaacgactt tcagtccccg acgcgccccg 500

cccaacccct acgatgaaga gggcgtccgc tggagggagc cggctgctgg 550

catgggtgct gtggctgcag gcctggcagg tggcagcccc atgcccaggt 600

gcctgcgtat gctacaatga gcccaaggtg acgacaagct gcccccagca 650

gggcctgcag gctgtgcccg tgggcatccc tgctgccagc cagcgcatct 700

tcctgcacgg caaccgcatc tcgcatgtgc cagctgccag cttccgtgcc 750

tgccgcaacc tcaccatcct gtggctgcac tcgaatgtgc tggcccgaat 800

tgatgcggct gccttcactg gcctggccct cctggagcag ctggacctca 850

gcgataatgc acagctccgg tctgtggacc ctgccacatt ccacggcctg 900

ggccgcctac acacgctgca cctggaccgc tgcggcctgc aggagctggg 950

cccggggctg ttccgcggcc tggctgccct gcagtacctc tacctgcagg 1000

acaacgcgct gcaggcactg cctgatgaca ccttccgcga cctgggcaac 1050

ctcacacacc tcttcctgca cggcaaccgc atctccagcg tgcccgagcg 1100

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cgccttccgt gggctgcaca gcctcgaccg tctcctactg caccagaacc 1150

gcgtggccca tgtgcacccg catgccttcc gtgaccttgg ccgcctcatg 1200

acactctatc tgtttgccaa caatctatca gcgctgccca ctgaggccct 1250

ggcccccctg cgtgccctgc agtacctgag gctcaacgac aacccctggg 1300

tgtgtgactg ccgggcacgc ccactctggg cctggctgca gaagttccgc 1350

ggctcctcct ccgaggtgcc ctgcagcctc ccgcaacgcc tggctggccg 1400

tgacctcaaa cgcctagctg ccaatgacct gcagggctgc gctgtggcca 1450

ccggcccctta ccatcccatc tggaccggca gggccaccga tgaggagccg 1500

ctggggcttc ccaagtgctg ccagccagat gccgctgaca aggcctcagt 1550

actggagcct ggaagaccag cttcggcagg caatgcgctg aagggacgcg 1600

tgccgcccgg tgacagcccg ccgggcaacg gctctggccc acggcacatc 1650

aatgactcac cctttgggac tctgcctggc tctgctgagc cccgctcac 1700

tgcagtgcgg cccgagggct ccgagccacc aggggttcccc acctcgggcc 1750

ctcgccggag gccaggctgt tcacgcaaga accgcacccg cagccactgc 1800

cgtctgggcc aggcaggcag cgggggtggc gggactggtg actcagaagg 1850

ctcaggtgcc ctacccagcc tcacctgcag cctcaccccc ctgggcctgg 1900

cgctggtgct gtggacagtg cttgggccct gctgaccccc agcggacaca 1950

agagcgtgct cagcagccag gtgtgtgtac atacggggtc tctctccacg 2000

ccgccaagcc agccgggcgg ccgacccgtg gggcaggcca ggccaggtcc 2050

tccctgatgg acgcctgccg cccgccaccc ccatctccac cccatcatgt 2100

ttacagggtt cggcggcagc gtttgttcca gaacgccgcc tcccacccag 2150

atcgcggtat atagagatat gcattttatt ttacttgtgt aaaaatatcg 2200

gacgacgtgg aataaagagc tcttttctta aaaaaa 2236
```

<210> 400
<211> 473
<212> PRT
<213> Homo sapiens

<400> 400

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Met Lys Arg Ala Ser Ala Gly Gly Ser Arg Leu Leu Ala Trp Val
  1               5                  10                  15

Leu Trp Leu Gln Ala Trp Gln Val Ala Ala Pro Cys Pro Gly Ala
                 20                  25                  30
```

```
Cys Val Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln
                35                  40                  45

Gln Gly Leu Gln Ala Val Pro Val Gly Ile Pro Ala Ala Ser Gln
                50                  55                  60

Arg Ile Phe Leu His Gly Asn Arg Ile Ser His Val Pro Ala Ala
                65                  70                  75

Ser Phe Arg Ala Cys Arg Asn Leu Thr Ile Leu Trp Leu His Ser
                80                  85                  90

Asn Val Leu Ala Arg Ile Asp Ala Ala Ala Phe Thr Gly Leu Ala
                95                 100                 105

Leu Leu Glu Gln Leu Asp Leu Ser Asp Asn Ala Gln Leu Arg Ser
               110                 115                 120

Val Asp Pro Ala Thr Phe His Gly Leu Gly Arg Leu His Thr Leu
               125                 130                 135

His Leu Asp Arg Cys Gly Leu Gln Glu Leu Gly Pro Gly Leu Phe
               140                 145                 150

Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr Leu Gln Asp Asn Ala
               155                 160                 165

Leu Gln Ala Leu Pro Asp Asp Thr Phe Arg Asp Leu Gly Asn Leu
               170                 175                 180

Thr His Leu Phe Leu His Gly Asn Arg Ile Ser Ser Val Pro Glu
               185                 190                 195

Arg Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu Leu His
               200                 205                 210

Gln Asn Arg Val Ala His Val His Pro His Ala Phe Arg Asp Leu
               215                 220                 225

Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Ala
               230                 235                 240

Leu Pro Thr Glu Ala Leu Ala Pro Leu Arg Ala Leu Gln Tyr Leu
               245                 250                 255

Arg Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro
               260                 265                 270

Leu Trp Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val
               275                 280                 285

Pro Cys Ser Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg
               290                 295                 300

Leu Ala Ala Asn Asp Leu Gln Gly Cys Ala Val Ala Thr Gly Pro
               305                 310                 315

Tyr His Pro Ile Trp Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu
```

```
                320                 325                 330

Gly Leu Pro Lys Cys Cys Gln Pro Asp Ala Ala Asp Lys Ala Ser
                335                 340                 345

Val Leu Glu Pro Gly Arg Pro Ala Ser Ala Gly Asn Ala Leu Lys
                350                 355                 360

Gly Arg Val Pro Pro Gly Asp Ser Pro Pro Gly Asn Gly Ser Gly
                365                 370                 375

Pro Arg His Ile Asn Asp Ser Pro Phe Gly Thr Leu Pro Gly Ser
                380                 385                 390

Ala Glu Pro Pro Leu Thr Ala Val Arg Pro Glu Gly Ser Glu Pro
                395                 400                 405

Pro Gly Phe Pro Thr Ser Gly Pro Arg Arg Arg Pro Gly Cys Ser
                410                 415                 420

Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly
                425                 430                 435

Ser Gly Gly Gly Gly Thr Gly Asp Ser Glu Gly Ser Gly Ala Leu
                440                 445                 450

Pro Ser Leu Thr Cys Ser Leu Thr Pro Leu Gly Leu Ala Leu Val
                455                 460                 465

Leu Trp Thr Val Leu Gly Pro Cys
                470
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<210> 401
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 401
tggctgccct gcagtacctc tacc 24

<210> 402
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 402
ccctgcaggt cattggcagc tagg 24

<210> 403
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 403
aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404
<211> 2738
<212> DNA
<213> Homo sapiens

<400> 404
ggaagtccac ggggagcttg gatgccaaag ggaggacggc tgggtcctct 50

ggagaggact actcactggc atatttctga ggtatctgta gaataaccac 100

agcctcagat actggggact ttacagtccc acagaaccgt cctcccagga 150

agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgcaga 200

caaaggcaag tcctttttc ctttctcctt ttgggcttat ctctggcggg 250

cgcggcggaa cctagaagct attctgtggt ggaggaaact gagggcagct 300

cctttgtcac caatttagca aaggacctgg gtctggagca gagggaattc 350

tccaggcggg gggttagggt tgtttccaga gggaacaaac tacatttgca 400

gctcaatcag gagaccgcgg atttgttgct aaatgagaaa ttggaccgtg 450

aggatctgtg cggtcacaca gagccctgtg tgctacgttt ccaagtgttg 500

ctagagagtc ccttcgagtt ttttcaagct gagctgcaag taatagacat 550

aaacgaccac tctccagtat ttctggacaa acaaatgttg gtgaaagtat 600

cagagagcag tcctcctggg actacgtttc ctctgaagaa tgccgaagac 650

ttagatgtag gccaaaacaa tattgagaac tatataatca gccccaactc 700

ctattttcgg gtcctcaccc gcaaacgcag tgatggcagg aaatacccag 750

agctggtgct ggacaaagcg ctggaccgag aggaagaagc tgagctcagg 800

ttaacactca cagcactgga tggtggctct ccgcccagat ctggcactgc 850

tcaggtctac atcgaagtcc tggatgtcaa cgataatgcc cctgaatttg 900

agcagccttt ctatagagtg cagatctctg aggacagtcc ggtaggcttc 950

ctggttgtga aggtctctgc cacggatgta gacacaggag tcaacggaga 1000

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gaaaaacttc agtcctatga agtcaatatt gaggcaagag atgctggaac 1150

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caggctgctg agcgagcgcg acgcggccaa gcacaggctg gtggtgctgg 2100
tcaaggacaa tggcgagcct ccgcgctcgg ccaccgccac gctgcacgtg 2150
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gtgcggctgt gtaggaggag cagggcggcc tcggtgggtc gctgcttggt 2350
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attttgtggc atttccatgc caatgtttat ttcccccaat ttgtgtgtat 2650

gtaatattgt acggatttac tcttgatttt tctcatgttc tttctccctt 2700

tgttttaaag tgaacattta cctttattcc tggttctt 2738

<210> 405
<211> 798
<212> PRT
<213> Homo sapiens

<400> 405
Met Glu Ala Ser Gly Lys Leu Ile Cys Arg Gln Arg Gln Val Leu
1 5 10 15

Phe Ser Phe Leu Leu Leu Gly Leu Ser Leu Ala Gly Ala Ala Glu
20 25 30

Pro Arg Ser Tyr Ser Val Val Glu Glu Thr Glu Gly Ser Ser Phe
35 40 45

Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe
50 55 60

Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His
65 70 75

Leu Gln Leu Asn Gln Glu Thr Ala Asp Leu Leu Leu Asn Glu Lys
80 85 90

Leu Asp Arg Glu Asp Leu Cys Gly His Thr Glu Pro Cys Val Leu
95 100 105

Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala
110 115 120

Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu
125 130 135

Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly
140 145 150

Thr Thr Phe Pro Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln
155 160 165

Asn Asn Ile Glu Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg
170 175 180

Val Leu Thr Arg Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu
185 190 195

Val Leu Asp Lys Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg
200 205 210

Leu Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly
215 220 225

Thr Ala Gln Val Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala

```
                230                 235                 240

Pro Glu Phe Glu Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp
                245                 250                 255

Ser Pro Val Gly Phe Leu Val Val Lys Val Ser Ala Thr Asp Val
                260                 265                 270

Asp Thr Gly Val Asn Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala
                275                 280                 285

Ser Glu Glu Ile Gly Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly
                290                 295                 300

Glu Ile Glu Leu Lys Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser
                305                 310                 315

Tyr Glu Val Asn Ile Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly
                320                 325                 330

Lys Cys Thr Val Leu Ile Gln Val Ile Asp Val Asn Asp His Ala
                335                 340                 345

Pro Glu Val Thr Met Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn
                350                 355                 360

Ala Pro Glu Thr Val Val Ala Leu Phe Ser Val Ser Asp Leu Asp
                365                 370                 375

Ser Gly Glu Asn Gly Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu
                380                 385                 390

Pro Phe Leu Leu Lys Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr
                395                 400                 405

Glu Arg Pro Leu Asp Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr
                410                 415                 420

Ile Thr Val Thr Asp Leu Gly Thr Pro Met Leu Ile Thr Gln Leu
                425                 430                 435

Asn Met Thr Val Leu Ile Ala Asp Val Asn Asp Asn Ala Pro Ala
                440                 445                 450

Phe Thr Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser
                455                 460                 465

Pro Ala Leu His Ile Arg Ser Val Ser Ala Thr Asp Arg Asp Ser
                470                 475                 480

Gly Thr Asn Ala Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp
                485                 490                 495

Pro His Leu Pro Leu Thr Ser Leu Val Ser Ile Asn Ala Asp Asn
                500                 505                 510

Gly His Leu Phe Ala Leu Arg Ser Leu Asp Tyr Glu Ala Leu Gln
                515                 520                 525
```

Gly Phe Gln Phe Arg Val Gly Ala Ser Asp His Gly Ser Pro Ala
530 535 540

Leu Ser Ser Glu Ala Leu Val Arg Val Val Val Leu Asp Ala Asn
545 550 555

Asp Asn Ser Pro Phe Val Leu Tyr Pro Leu Gln Asn Gly Ser Ala
560 565 570

Pro Cys Thr Glu Leu Val Pro Arg Ala Ala Glu Pro Gly Tyr Leu
575 580 585

Val Thr Lys Val Val Ala Val Asp Gly Asp Ser Gly Gln Asn Ala
590 595 600

Trp Leu Ser Tyr Gln Leu Leu Lys Ala Thr Glu Leu Gly Leu Phe
605 610 615

Gly Val Trp Ala His Asn Gly Glu Val Arg Thr Ala Arg Leu Leu
620 625 630

Ser Glu Arg Asp Ala Ala Lys His Arg Leu Val Val Leu Val Lys
635 640 645

Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala Thr Leu His Val
650 655 660

Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu Pro Glu
665 670 675

Ala Ala Pro Thr Gln Ala Gln Ala Asp Leu Leu Thr Val Tyr Leu
680 685 690

Val Val Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser Val
695 700 705

Leu Leu Phe Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala
710 715 720

Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His
725 730 735

Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln
740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys
755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly
770 775 780

Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe
785 790 795

Asn Ile Gln

<210> 406

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 406
ctgagaacgc gcctgaaact gtg 23

<210> 407
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 407
agcgttgtca ttgacatcgg cg 22

<210> 408
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 408
ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409
<211> 1379
<212> DNA
<213> Homo sapiens

<400> 409
acccacgcgt ccgcccacgc gtccgcccac gcgtccgccc acgcgtccgc 50

gcgtagccgt gcgccgattg cctctcggcc tgggcaatgg tcccggctgc 100

cggtcgacga ccgccccgcg tcatgcggct cctcggctgg tggcaagtat 150

tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200

agtggtcgct tatggtcaga ggagcagcct gctcaccctc tccaggtggg 250

ggctgtgtac ctgggtgagg aggagctcct gcatgacccg atgggccagg 300

acagggcagc agaagaggcc aatgcggtgc tggggctgga cacccaaggc 350

gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400

gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450

caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500 cacttccctg acagagaaga ggagtattac acagagccag aagtggcgga 550

atctgacgca gccccgacag aggactccaa taacactgaa agtctgaaat 600

ccccaaaggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650

actctgaaaa ttttaaatat gtcacaggac cttatggatt ttctgaaccc 700

aaacggtagt gactgtactc tagtcctgtt ttacaccccg tggtgccgct 750

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caggtttggc accgtagctg ttcctaatat tttattattt caaggagcta 900

aaccaatggc cagatttaat catacagatc gaacactgga aacactgaaa 950

atcttcattt ttaatcagac aggtatagaa gccaagaaga atgtggtggt 1000

aactcaagcc gaccaaatag gccctcttcc cagcactttg ataaaaagtg 1050

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tatgctacca ttcgaactga gagtattcgg tggctaattc caggacaaga 1150

gcaggaacat gtggagtagt gatggtctga aagaagttgg aaagaggaac 1200

ttcaatcctt cgtttcagaa attagtgcta cagtttcata cattttctcc 1250

agtgacgtgt tgacttgaaa cttcaggcag attaaaagaa tcatttgttg 1300

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caataagcaa atgcaaaaat attcaatag 1379

<210> 410
<211> 360
<212> PRT
<213> Homo sapiens

<400> 410

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Met Val Pro Ala Ala Gly Arg Arg Pro Pro Arg Val Met Arg Leu
 1               5                  10                  15

Leu Gly Trp Trp Gln Val Leu Leu Trp Val Leu Gly Leu Pro Val
                20                  25                  30

Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser Glu
                35                  40                  45

Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly
                50                  55                  60

Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala
                65                  70                  75

Glu Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His
```

80 85 90

Met Val Met Leu Ser Val Ile Pro Gly Glu Ala Glu Asp Lys Val
95 100 105

Ser Ser Glu Pro Ser Gly Val Thr Cys Gly Ala Gly Gly Ala Glu
110 115 120

Asp Ser Arg Cys Asn Val Arg Glu Ser Leu Phe Ser Leu Asp Gly
125 130 135

Ala Gly Ala His Phe Pro Asp Arg Glu Glu Glu Tyr Tyr Thr Glu
140 145 150

Pro Glu Val Ala Glu Ser Asp Ala Ala Pro Thr Glu Asp Ser Asn
155 160 165

Asn Thr Glu Ser Leu Lys Ser Pro Lys Val Asn Cys Glu Glu Arg
170 175 180

Asn Ile Thr Gly Leu Glu Asn Phe Thr Leu Lys Ile Leu Asn Met
185 190 195

Ser Gln Asp Leu Met Asp Phe Leu Asn Pro Asn Gly Ser Asp Cys
200 205 210

Thr Leu Val Leu Phe Tyr Thr Pro Trp Cys Arg Phe Ser Ala Ser
215 220 225

Leu Ala Pro His Phe Asn Ser Leu Pro Arg Ala Phe Pro Ala Leu
230 235 240

His Phe Leu Ala Leu Asp Ala Ser Gln His Ser Ser Leu Ser Thr
245 250 255

Arg Phe Gly Thr Val Ala Val Pro Asn Ile Leu Leu Phe Gln Gly
260 265 270

Ala Lys Pro Met Ala Arg Phe Asn His Thr Asp Arg Thr Leu Glu
275 280 285

Thr Leu Lys Ile Phe Ile Phe Asn Gln Thr Gly Ile Glu Ala Lys
290 295 300

Lys Asn Val Val Val Thr Gln Ala Asp Gln Ile Gly Pro Leu Pro
305 310 315

Ser Thr Leu Ile Lys Ser Val Asp Trp Leu Leu Val Phe Ser Leu
320 325 330

Phe Phe Leu Ile Ser Phe Ile Met Tyr Ala Thr Ile Arg Thr Glu
335 340 345

Ser Ile Arg Trp Leu Ile Pro Gly Gln Glu Gln Glu His Val Glu
350 355 360

<210> 411
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 411
cacagagcca gaagtggcgg aatc 24

<210> 412
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 412
ccacatgttc ctgctcttgt cctgg 25

<210> 413
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 413
cggtagtgac tgtactctag tcctgtttta caccccgtgg tgccg 45

<210> 414
<211> 1196
<212> DNA
<213> Homo sapiens

<400> 414
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ggctcggcgc gcgggctctt cctctttggc cagcccgact tctcctacaa 150

gcgcagcaat tgcaagccca tcccggtcaa cctgcagctg tgccacggca 200

tcgaatacca gaacatgcgg ctgcccaacc tgctgggcca cgagaccatg 250

aaggaggtgc tggagcaggc cggcgcttgg atcccgctgg tcatgaagca 300

gtgccacccg gacaccaaga agttcctgtg ctcgctcttc gcccccgtct 350

gcctcgatga cctagacgag accatccagc catgccactc gctctgcgtg 400

caggtgaagg accgctgcgc cccggtcatg tccgccttcg gcttcccctg 450

gcccgacatg cttgagtgcg accgtttccc ccaggacaac gacctttgca 500

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gctgtggctc aaagacagct tgcagtgcac ctgtgaggag atgaacgaca 800

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gaatcttgta gaaatattca aactaataaa atcatgaata ttttaa 1196

<210> 415
<211> 295
<212> PRT
<213> Homo sapiens

<400> 415

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Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Leu Phe Leu Ala Ser
 1               5                  10                  15

His Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln
                20                  25                  30

Pro Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Val
                35                  40                  45

Asn Leu Gln Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu
                50                  55                  60

Pro Asn Leu Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln
                65                  70                  75

Ala Gly Ala Trp Ile Pro Leu Val Met Lys Gln Cys His Pro Asp
                80                  85                  90

Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala Pro Val Cys Leu Asp
                95                 100                 105

Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser Leu Cys Val Gln
               110                 115                 120

Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe Gly Phe Pro
               125                 130                 135
```

```
Trp Pro Asp Met Leu Glu Cys Asp Arg Phe Pro Gln Asp Asn Asp
                140                 145                 150

Leu Cys Ile Pro Leu Ala Ser Ser Asp His Leu Leu Pro Ala Thr
                155                 160                 165

Glu Glu Ala Pro Lys Val Cys Glu Ala Cys Lys Asn Lys Asn Asp
                170                 175                 180

Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn Asp Phe Ala
                185                 190                 195

Leu Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg Asp Thr
                200                 205                 210

Lys Ile Ile Leu Glu Thr Lys Ser Lys Thr Ile Tyr Lys Leu Asn
                215                 220                 225

Gly Val Ser Glu Arg Asp Leu Lys Lys Ser Val Leu Trp Leu Lys
                230                 235                 240

Asp Ser Leu Gln Cys Thr Cys Glu Glu Met Asn Asp Ile Asn Ala
                245                 250                 255

Pro Tyr Leu Val Met Gly Gln Lys Gln Gly Gly Glu Leu Val Ile
                260                 265                 270

Thr Ser Val Lys Arg Trp Gln Lys Gly Gln Arg Glu Phe Lys Arg
                275                 280                 285

Ile Ser Arg Ser Ile Arg Lys Leu Gln Cys
                290                 295
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<210> 416
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 416
cctggctcgc tgctgctgct c 21

<210> 417
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 417
cctcacaggt gcactgcaag ctgtc 25

<210> 418
<211> 47
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 418
ctcttcctct ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419
<211> 1830
<212> DNA
<213> Homo sapiens

<400> 419
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ccgagccccg ggccctgtgc gcgcagcggg gccaccgcac ctacgcgcgc 100

cgctgggtgt tcctgctcgc gatcagcctg ctcaactgct ccaacgccac 150

gctgtggctc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200

tcctgtccat ggagcagatc aactggctgt cactggtcta cctcgtggta 250

tccaccccat ttggcgtggc ggccatctgg atcctggact ccgtcgggct 300

ccgtgcggcg accatcctgg gtgcgtggct gaactttgcc gggagtgtgc 350

tacgcatggt gccctgcatg gttgttggga cccaaaaccc atttgccttc 400

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cggccaacat gctcgccacc atgtcgaacc ctctgggcgt ccttgtggcc 550

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gaacaaggcc tatgtcatcc tggctgtgtg cttgggggga atgatcggga 800

tctctgccag cttctcagcc ctcctggagc agatcctctg tgcaagcggc 850

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ccctttgccc tggtgtccca gctgcaggga cagacccttg ccctggctgc 1050

cacctgctcg ctgctcgggc tgtttggctt ctcggtgggc cccgtggcca 1100

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aatgacggca ctgactgtgc gacgctcgga gccgtccttg tccacctgcc 1250

agcaggggga ggatccactt gactggacag tgtctctgct gctgatggcc 1300

ggcctgtgca ccttcttcag ctgcatcctg gcggtcttct tccacacccc 1350

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ccgtgggcgg cgcagactca gggccgggtg tggaccgagg gggagcagga 1450

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tcccgccccg gcagactcgc aggcagggtc caagcgtcca ggtttattga 1650

cccggctggg tctcactcct ccttctcctc cccgtgggtg atcacgtagc 1700

tgagcgcctt gtagtccagg ttgcccgcca catcgatgga ggcgaactgg 1750

aacatctggt ccacctgcgg gcgggggcga aagggctcct tgcgggctcc 1800

gggagcgaat tacaagcgcg cacctgaaaa 1830

<210> 420
<211> 560
<212> PRT
<213> Homo sapiens

<400> 420
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1               5                   10                  15

Ala Leu Cys Ala Gln Arg Gly His Arg Thr Tyr Ala Arg Arg Trp
            20                  25                  30

Val Phe Leu Leu Ala Ile Ser Leu Leu Asn Cys Ser Asn Ala Thr
        35                  40                  45

Leu Trp Leu Ser Phe Ala Pro Val Ala Asp Val Ile Ala Glu Asp
    50                  55                  60

Leu Val Leu Ser Met Glu Gln Ile Asn Trp Leu Ser Leu Val Tyr
65                  70                  75

Leu Val Val Ser Thr Pro Phe Gly Val Ala Ala Ile Trp Ile Leu
                80                  85                  90

Asp Ser Val Gly Leu Arg Ala Ala Thr Ile Leu Gly Ala Trp Leu
            95                  100                 105

Asn Phe Ala Gly Ser Val Leu Arg Met Val Pro Cys Met Val Val
```

```
                110                 115                 120

Gly Thr Gln Asn Pro Phe Ala Phe Leu Met Gly Gly Gln Ser Leu
                125                 130                 135

Cys Ala Leu Ala Gln Ser Leu Val Ile Phe Ser Pro Ala Lys Leu
                140                 145                 150

Ala Ala Leu Trp Phe Pro Glu His Gln Arg Ala Thr Ala Asn Met
                155                 160                 165

Leu Ala Thr Met Ser Asn Pro Leu Gly Val Leu Val Ala Asn Val
                170                 175                 180

Leu Ser Pro Val Leu Val Lys Lys Gly Glu Asp Ile Pro Leu Met
                185                 190                 195

Leu Gly Val Tyr Thr Ile Pro Ala Gly Val Val Cys Leu Leu Ser
                200                 205                 210

Thr Ile Cys Leu Trp Glu Ser Val Pro Pro Thr Pro Pro Ser Ala
                215                 220                 225

Gly Ala Ala Ser Ser Thr Ser Glu Lys Phe Leu Asp Gly Leu Lys
                230                 235                 240

Leu Gln Leu Met Trp Asn Lys Ala Tyr Val Ile Leu Ala Val Cys
                245                 250                 255

Leu Gly Gly Met Ile Gly Ile Ser Ala Ser Phe Ser Ala Leu Leu
                260                 265                 270

Glu Gln Ile Leu Cys Ala Ser Gly His Ser Ser Gly Phe Ser Gly
                275                 280                 285

Leu Cys Gly Ala Leu Phe Ile Thr Phe Gly Ile Leu Gly Ala Leu
                290                 295                 300

Ala Leu Gly Pro Tyr Val Asp Arg Thr Lys His Phe Thr Glu Ala
                305                 310                 315

Thr Lys Ile Gly Leu Cys Leu Phe Ser Leu Ala Cys Val Pro Phe
                320                 325                 330

Ala Leu Val Ser Gln Leu Gln Gly Gln Thr Leu Ala Leu Ala Ala
                335                 340                 345

Thr Cys Ser Leu Leu Gly Leu Phe Gly Phe Ser Val Gly Pro Val
                350                 355                 360

Ala Met Glu Leu Ala Val Glu Cys Ser Phe Pro Val Gly Glu Gly
                365                 370                 375

Ala Ala Thr Gly Met Ile Phe Val Leu Gly Gln Ala Glu Gly Ile
                380                 385                 390

Leu Ile Met Leu Ala Met Thr Ala Leu Thr Val Arg Arg Ser Glu
                395                 400                 405
```

```
Pro Ser Leu Ser Thr Cys Gln Gln Gly Glu Asp Pro Leu Asp Trp
                410                 415                 420

Thr Val Ser Leu Leu Leu Met Ala Gly Leu Cys Thr Phe Phe Ser
                425                 430                 435

Cys Ile Leu Ala Val Phe Phe His Thr Pro Tyr Arg Arg Leu Gln
                440                 445                 450

Ala Glu Ser Gly Glu Pro Pro Ser Thr Arg Asn Ala Val Gly Gly
                455                 460                 465

Ala Asp Ser Gly Pro Gly Val Asp Arg Gly Gly Ala Gly Arg Ala
                470                 475                 480

Gly Val Leu Gly Pro Ser Thr Ala Thr Pro Glu Cys Thr Ala Arg
                485                 490                 495

Gly Ala Ser Leu Glu Asp Pro Arg Gly Pro Gly Ser Pro His Pro
                500                 505                 510

Ala Cys His Arg Ala Thr Pro Arg Ala Gln Gly Pro Ala Ala Thr
                515                 520                 525

Asp Ala Pro Ser Arg Pro Gly Arg Leu Ala Gly Arg Val Gln Ala
                530                 535                 540

Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser
                545                 550                 555

Pro Trp Val Ile Thr
                560
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<210> 421
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 421
agcttctcag ccctcctgga gcag 24

<210> 422
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 422
cgggtcaata aacctggacg cttgg 25

<210> 423
<211> 43
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 423
tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424
<211> 4313
<212> DNA
<213> Homo sapiens

<400> 424
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ccatcatttg ctgaagtgga ccaactagtt ccccagtagg gggtctcccc 100

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tggccttgcc ttggggtcct gcttgtttca taatcatcta actatgggac 200

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gtgctggaca tcaatgacca ccagccacgg tttcccaaag gcgagcagga 750

gctggaaatc tctgagagcg cctctctgcg aacccggatc cccctggaca 800

gagctcttga cccagacaca ggccctaaca ccctgcacac ctacactctg 850

tctcccagtg agcactttgc cttggatgtc attgtgggcc ctgatgagac 900

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tcaggtacca gcttggtcaa ggtcaacgtc ttggactcca atgacaatag 1050

ccctgcgttt gctgagagtt cactggcact ggaaatccaa gaagatgctg 1100

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gctggacacc ttcagtattg atgccaagac aggccaggtc attctgcgtc 1250

gacctctaga ctatgaaaag aaccctgcct acgaggtgga tgttcaggca 1300

agggacctgg gtcccaatcc tatcccagcc cattgcaaag ttctcatcaa 1350

ggttctggat gtcaatgaca acatcccaag catccacgtc acatgggcct 1400

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acggtttgtg gctgagataa gtgtttcctg gcaaaacata tgtggagcac 4150

aaagggtcag tcctctggca gaacagatgc cacggagtat cacaggcagg 4200

aaagggtggc cttcttgggt agcaggagtc aggggggctgt accctggggg 4250

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<210> 425
<211> 1184
<212> PRT
<213> Homo sapiens

<400> 425

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Met Met Gln Leu Leu Gln Leu Leu Leu Gly Leu Leu Gly Pro Gly
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Gly Tyr Leu Phe Leu Leu Gly Asp Cys Gln Glu Val Thr Thr Leu
                20                  25                  30

Thr Val Lys Tyr Gln Val Ser Glu Glu Val Pro Ser Gly Thr Val
                35                  40                  45

Ile Gly Lys Leu Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg
                50                  55                  60

Gln Ala Gly Ala Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu
                65                  70                  75

Pro Ile Gln Val Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg
                80                  85                  90

Arg Leu Asp Arg Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu
                95                 100                 105

Val Ser Phe Asp Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His
               110                 115                 120

Val Glu Ile Gln Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe
               125                 130                 135

Pro Lys Gly Glu Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu
               140                 145                 150

Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly
               155                 160                 165

Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe
               170                 175                 180

Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu
               185                 190                 195
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Leu Ile Val Val Lys Glu Leu Asp Arg Glu Ile His Ser Phe Phe
                200                 205                 210

Asp Leu Val Leu Thr Ala Tyr Asp Asn Gly Asn Pro Pro Lys Ser
                215                 220                 225

Gly Thr Ser Leu Val Lys Val Asn Val Leu Asp Ser Asn Asp Asn
                230                 235                 240

Ser Pro Ala Phe Ala Glu Ser Ser Leu Ala Leu Glu Ile Gln Glu
                245                 250                 255

Asp Ala Ala Pro Gly Thr Leu Leu Ile Lys Leu Thr Ala Thr Asp
                260                 265                 270

Pro Asp Gln Gly Pro Asn Gly Glu Val Glu Phe Phe Leu Ser Lys
                275                 280                 285

His Met Pro Pro Glu Val Leu Asp Thr Phe Ser Ile Asp Ala Lys
                290                 295                 300

Thr Gly Gln Val Ile Leu Arg Arg Pro Leu Asp Tyr Glu Lys Asn
                305                 310                 315

Pro Ala Tyr Glu Val Asp Val Gln Ala Arg Asp Leu Gly Pro Asn
                320                 325                 330

Pro Ile Pro Ala His Cys Lys Val Leu Ile Lys Val Leu Asp Val
                335                 340                 345

Asn Asp Asn Ile Pro Ser Ile His Val Thr Trp Ala Ser Gln Pro
                350                 355                 360

Ser Leu Val Ser Glu Ala Leu Pro Lys Asp Ser Phe Ile Ala Leu
                365                 370                 375

Val Met Ala Asp Asp Leu Asp Ser Gly His Asn Gly Leu Val His
                380                 385                 390

Cys Trp Leu Ser Gln Glu Leu Gly His Phe Arg Leu Lys Arg Thr
                395                 400                 405

Asn Gly Asn Thr Tyr Met Leu Leu Thr Asn Ala Thr Leu Asp Arg
                410                 415                 420

Glu Gln Trp Pro Lys Tyr Thr Leu Thr Leu Leu Ala Gln Asp Gln
                425                 430                 435

Gly Leu Gln Pro Leu Ser Ala Lys Lys Gln Leu Ser Ile Gln Ile
                440                 445                 450

Ser Asp Ile Asn Asp Asn Ala Pro Val Phe Glu Lys Ser Arg Tyr
                455                 460                 465

Glu Val Ser Thr Arg Glu Asn Asn Leu Pro Ser Leu His Leu Ile
                470                 475                 480

Thr Ile Lys Ala His Asp Ala Asp Leu Gly Ile Asn Gly Lys Val
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485 490 495

Ser Tyr Arg Ile Gln Asp Ser Pro Val Ala His Leu Val Ala Ile
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Asp Ser Asn Thr Gly Glu Val Thr Ala Gln Arg Ser Leu Asn Tyr
515 520 525

Glu Glu Met Ala Gly Phe Glu Phe Gln Val Ile Ala Glu Asp Ser
530 535 540

Gly Gln Pro Met Leu Ala Ser Ser Val Ser Val Trp Val Ser Leu
545 550 555

Leu Asp Ala Asn Asp Asn Ala Pro Glu Val Val Gln Pro Val Leu
560 565 570

Ser Asp Gly Lys Ala Ser Leu Ser Val Leu Val Asn Ala Ser Thr
575 580 585

Gly His Leu Leu Val Pro Ile Glu Thr Pro Asn Gly Leu Gly Pro
590 595 600

Ala Gly Thr Asp Thr Pro Pro Leu Ala Thr His Ser Ser Arg Pro
605 610 615

Phe Leu Leu Thr Thr Ile Val Ala Arg Asp Ala Asp Ser Gly Ala
620 625 630

Asn Gly Glu Pro Leu Tyr Ser Ile Arg Asn Gly Asn Glu Ala His
635 640 645

Leu Phe Ile Leu Asn Pro His Thr Gly Gln Leu Phe Val Asn Val
650 655 660

Thr Asn Ala Ser Ser Leu Ile Gly Ser Glu Trp Glu Leu Glu Ile
665 670 675

Val Val Glu Asp Gln Gly Ser Pro Pro Leu Gln Thr Arg Ala Leu
680 685 690

Leu Arg Val Met Phe Val Thr Ser Val Asp His Leu Arg Asp Ser
695 700 705

Ala Arg Lys Pro Gly Ala Leu Ser Met Ser Met Leu Thr Val Ile
710 715 720

Cys Leu Ala Val Leu Leu Gly Ile Phe Gly Leu Ile Leu Ala Leu
725 730 735

Phe Met Ser Ile Cys Arg Thr Glu Lys Lys Asp Asn Arg Ala Tyr
740 745 750

Asn Cys Arg Glu Ala Glu Ser Thr Tyr Arg Gln Gln Pro Lys Arg
755 760 765

Pro Gln Lys His Ile Gln Lys Ala Asp Ile His Leu Val Pro Val
770 775 780

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Leu Arg Gly Gln Ala Gly Glu Pro Cys Glu Val Gly Gln Ser His
                785                 790                 795

Lys Asp Val Asp Lys Glu Ala Met Met Glu Ala Gly Trp Asp Pro
                800                 805                 810

Cys Leu Gln Ala Pro Phe His Leu Thr Pro Thr Leu Tyr Arg Thr
                815                 820                 825

Leu Arg Asn Gln Gly Asn Gln Gly Ala Pro Ala Glu Ser Arg Glu
                830                 835                 840

Val Leu Gln Asp Thr Val Asn Leu Leu Phe Asn His Pro Arg Gln
                845                 850                 855

Arg Asn Ala Ser Arg Glu Asn Leu Asn Leu Pro Glu Pro Gln Pro
                860                 865                 870

Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser
                875                 880                 885

Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro
                890                 895                 900

Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His
                905                 910                 915

Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln
                920                 925                 930

Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu
                935                 940                 945

Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln
                950                 955                 960

Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln
                965                 970                 975

Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly
                980                 985                 990

Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg
                995                1000                1005

Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp
               1010                1015                1020

Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu
               1025                1030                1035

Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu
               1040                1045                1050

Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu
               1055                1060                1065

Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala
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                1070                1075                1080

Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala
                1085                1090                1095

Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val
                1100                1105                1110

Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser
                1115                1120                1125

Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser
                1130                1135                1140

Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala
                1145                1150                1155

Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr
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Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Ser Arg Cys Leu
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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 426
gtaagcacat gcctccagag gtgc 24

<210> 427
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 427
gtgacgtgga tgcttgggat gttg 24

<210> 428
<211> 50
<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 428
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<210> 429
<211> 2037

<212> DNA
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tgagtttcct catcgactcc agcatcatga ttacctccca gatactattt 200

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gatcctggtt ttcatggtgc ctttttacat tggctatttt attgtgagca 450

atatccgact actgcataaa caacgactgc ttttttcctg tctcttatgg 500

ctgaccttta tgtatttctt ctggaaacta ggagatccct ttcccattct 550

cagcccaaaa catgggatct tatccataga acagctcatc agccgggttg 600

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taagcaaaaa gaaaaggatg gcaatggcac ggagaacaat gttccagaag 800

ggggaagtgc ataacaaacc atcaggtttc tggggaatga taaaaagtgt 850

taccacttca gcatcaggaa gtgaaaatct tactcttatt caacaggaag 900

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ccgccatggc ccaacttgtt tattgcagct tataatg 2037

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<212> PRT
<213> Homo sapiens

<400> 430

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Leu	Phe	Phe	Gly	Phe	Gly	Trp	Leu	Phe	Phe	Met	Arg	Gln	Leu	Phe
				20					25					30
Lys	Asp	Tyr	Glu	Ile	Arg	Gln	Tyr	Val	Val	Gln	Val	Ile	Phe	Ser
				35					40					45
Val	Thr	Phe	Ala	Phe	Ser	Cys	Thr	Met	Phe	Glu	Leu	Ile	Ile	Phe
				50					55					60
Glu	Ile	Leu	Gly	Val	Leu	Asn	Ser	Ser	Ser	Arg	Tyr	Phe	His	Trp
				65					70					75
Lys	Met	Asn	Leu	Cys	Val	Ile	Leu	Leu	Ile	Leu	Val	Phe	Met	Val
				80					85					90
Pro	Phe	Tyr	Ile	Gly	Tyr	Phe	Ile	Val	Ser	Asn	Ile	Arg	Leu	Leu
				95					100					105
His	Lys	Gln	Arg	Leu	Leu	Phe	Ser	Cys	Leu	Leu	Trp	Leu	Thr	Phe
				110					115					120

Met Tyr Phe Phe Trp Lys Leu Gly Asp Pro Phe Pro Ile Leu Ser
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Pro Lys His Gly Ile Leu Ser Ile Glu Gln Leu Ile Ser Arg Val
140 145 150

Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu Ser Gly Phe Gly
155 160 165

Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe Leu Arg Asn
170 175 180

Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu Leu Gln
185 190 195

Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met Ala
200 205 210

Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser
215 220 225

Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly
230 235 240

Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu
245 250 255

Glu Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala
260 265 270

Thr Lys Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr
275 280 285

Phe Asn Phe Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys
290 295 300

Ile Phe Met Ala Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys
305 310 315

Thr Asp Pro Val Thr Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu
320 325 330

Gly Ile Gln Phe Asp Val Lys Phe Trp Ser Gln His Ile Ser Phe
335 340 345

Ile Leu Val Gly Ile Ile Ile Val Thr Ser Ile Arg Gly Leu Leu
350 355 360

Ile Thr Leu Thr Lys Phe Phe Tyr Ala Ile Ser Ser Ser Lys Ser
365 370 375

Ser Asn Val Ile Val Leu Leu Leu Ala Gln Ile Met Gly Met Tyr
380 385 390

Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser Met Pro Leu Glu
395 400 405

Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu Gln Phe Asn

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                410                 415                 420

Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser Ala Leu
                425                 430                 435

Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro Glu
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Lys Gln Met Ala Pro
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<210> 431
<211> 407
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 81, 113, 157, 224, 297
<223> unknown base

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ttgtacnggt gatcttctcc gtgacgtttg ccatttcttg caccatgttt 200

gagctcatca tctttgaaat cttnggagta ttgaatagca gctcccgtta 250

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tggtgccttt ttacattggc tattttattg tgagcaatat ccgactactg 350

cataaacaac gactgctttt ttcctgtctc ttatggctga cctttatgta 400

tttccag 407

<210> 432
<211> 457
<212> DNA
<213> Homo sapiens

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<221> unsure
<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434
<223> unknown base

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tattttttgg atttggggta gntttttttc atgcgccaat tgtttaaaga 150

ctatgagata cgtcagtatg ttgtacaggt gatnttntcc gtgacgtttg 200 cattttcttg caccatgttt gagctcatca tntttgaaat nttaggagta 250

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tctgctgatc ctggttttca tggtgccttt ttacattggc tattttattg 350

tgagcaatat ccgactactg cataaacaac gactgctttt ttcctgtctn 400

ttatggctga cctttatgta tttnttntgg aaantaggag atccctttcc 450

cattctc 457

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<213> Artificial Sequence

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<400> 433
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<210> 434
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 434
tcgttgttta tgcagtagtc gg 22

<210> 435
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<212> DNA
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<210> 436
<211> 3951
<212> DNA
<213> Homo sapiens

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tcctcccacc caacttcccc ttagagtgct gtgagatgag agtgggtaaa 3650

tcagggacag ggccatgggg tagggtgaga agggcagggg tgtcctgatg 3700

caaaggtggg gagaagggat cctaatccct tcctctccca ttcaccctgt 3750

gtaacaggac cccaaggacc tgcctccccg gaagtgcctt aacctagagg 3800

gtcggggagg aggttgtgtc actgactcag gctgctcctt ctctagtttc 3850

ccctctcatc tgaccttagt ttgctgccat cagtctagtg gtttcgtggt 3900

ttcgtctatt tattaaaaaa tatttgagaa caaaaaaaaa aaaaaaaaaa 3950

a 3951

<210> 437
<211> 1141
<212> PRT
<213> Homo sapiens

<400> 437
Met Ala Gly Ala Arg Ser Arg Asp Pro Trp Gly Ala Ser Gly Ile
1 5 10 15

Cys Tyr Leu Phe Gly Ser Leu Leu Val Glu Leu Leu Phe Ser Arg
20 25 30

Ala Val Ala Phe Asn Leu Asp Val Met Gly Ala Leu Arg Lys Glu
35 40 45

Gly Glu Pro Gly Ser Leu Phe Gly Phe Ser Val Ala Leu His Arg
50 55 60

Gln Leu Gln Pro Arg Pro Gln Ser Trp Leu Leu Val Gly Ala Pro
65 70 75

Gln Ala Leu Ala Leu Pro Gly Gln Gln Ala Asn Arg Thr Gly Gly

80 85 90

Leu Phe Ala Cys Pro Leu Ser Leu Glu Glu Thr Asp Cys Tyr Arg
95 100 105

Val Asp Ile Asp Gln Gly Ala Asp Met Gln Lys Glu Ser Lys Glu
110 115 120

Asn Gln Trp Leu Gly Val Ser Val Arg Ser Gln Gly Pro Gly Gly
125 130 135

Lys Ile Val Thr Cys Ala His Arg Tyr Glu Ala Arg Gln Arg Val
140 145 150

Asp Gln Ile Leu Glu Thr Arg Asp Met Ile Gly Arg Cys Phe Val
155 160 165

Leu Ser Gln Asp Leu Ala Ile Arg Asp Glu Leu Asp Gly Gly Glu
170 175 180

Trp Lys Phe Cys Glu Gly Arg Pro Gln Gly His Glu Gln Phe Gly
185 190 195

Phe Cys Gln Gln Gly Thr Ala Ala Ala Phe Ser Pro Asp Ser His
200 205 210

Tyr Leu Leu Phe Gly Ala Pro Gly Thr Tyr Asn Trp Lys Gly Thr
215 220 225

Ala Arg Val Glu Leu Cys Ala Gln Gly Ser Ala Asp Leu Ala His
230 235 240

Leu Asp Asp Gly Pro Tyr Glu Ala Gly Gly Glu Lys Glu Gln Asp
245 250 255

Pro Arg Leu Ile Pro Val Pro Ala Asn Ser Tyr Phe Gly Phe Ser
260 265 270

Ile Asp Ser Gly Lys Gly Leu Val Arg Ala Glu Glu Leu Ser Phe
275 280 285

Val Ala Gly Ala Pro Arg Ala Asn His Lys Gly Ala Val Val Ile
290 295 300

Leu Arg Lys Asp Ser Ala Ser Arg Leu Val Pro Glu Val Met Leu
305 310 315

Ser Gly Glu Arg Leu Thr Ser Gly Phe Gly Tyr Ser Leu Ala Val
320 325 330

Ala Asp Leu Asn Ser Asp Gly Trp Pro Asp Leu Ile Val Gly Ala
335 340 345

Pro Tyr Phe Phe Glu Arg Gln Glu Glu Leu Gly Gly Ala Val Tyr
350 355 360

Val Tyr Leu Asn Gln Gly Gly His Trp Ala Gly Ile Ser Pro Leu
365 370 375

Arg Leu Cys Gly Ser Pro Asp Ser Met Phe Gly Ile Ser Leu Ala
380 385 390

Val Leu Gly Asp Leu Asn Gln Asp Gly Phe Pro Asp Ile Ala Val
395 400 405

Gly Ala Pro Phe Asp Gly Asp Gly Lys Val Phe Ile Tyr His Gly
410 415 420

Ser Ser Leu Gly Val Val Ala Lys Pro Ser Gln Val Leu Glu Gly
425 430 435

Glu Ala Val Gly Ile Lys Ser Phe Gly Tyr Ser Leu Ser Gly Ser
440 445 450

Leu Asp Met Asp Gly Asn Gln Tyr Pro Asp Leu Leu Val Gly Ser
455 460 465

Leu Ala Asp Thr Ala Val Leu Phe Arg Ala Arg Pro Ile Leu His
470 475 480

Val Ser His Glu Val Ser Ile Ala Pro Arg Ser Ile Asp Leu Glu
485 490 495

Gln Pro Asn Cys Ala Gly Gly His Ser Val Cys Val Asp Leu Arg
500 505 510

Val Cys Phe Ser Tyr Ile Ala Val Pro Ser Ser Tyr Ser Pro Thr
515 520 525

Val Ala Leu Asp Tyr Val Leu Asp Ala Asp Thr Asp Arg Arg Leu
530 535 540

Arg Gly Gln Val Pro Arg Val Thr Phe Leu Ser Arg Asn Leu Glu
545 550 555

Glu Pro Lys His Gln Ala Ser Gly Thr Val Trp Leu Lys His Gln
560 565 570

His Asp Arg Val Cys Gly Asp Ala Met Phe Gln Leu Gln Glu Asn
575 580 585

Val Lys Asp Lys Leu Arg Ala Ile Val Val Thr Leu Ser Tyr Ser
590 595 600

Leu Gln Thr Pro Arg Leu Arg Arg Gln Ala Pro Gly Gln Gly Leu
605 610 615

Pro Pro Val Ala Pro Ile Leu Asn Ala His Gln Pro Ser Thr Gln
620 625 630

Arg Ala Glu Ile His Phe Leu Lys Gln Gly Cys Gly Glu Asp Lys
635 640 645

Ile Cys Gln Ser Asn Leu Gln Leu Val His Ala Arg Phe Cys Thr
650 655 660

Arg Val Ser Asp Thr Glu Phe Gln Pro Leu Pro Met Asp Val Asp

665 670 675

Gly Thr Thr Ala Leu Phe Ala Leu Ser Gly Gln Pro Val Ile Gly
680 685 690

Leu Glu Leu Met Val Thr Asn Leu Pro Ser Asp Pro Ala Gln Pro
695 700 705

Gln Ala Asp Gly Asp Asp Ala His Glu Ala Gln Leu Leu Val Met
710 715 720

Leu Pro Asp Ser Leu His Tyr Ser Gly Val Arg Ala Leu Asp Pro
725 730 735

Ala Glu Lys Pro Leu Cys Leu Ser Asn Glu Asn Ala Ser His Val
740 745 750

Glu Cys Glu Leu Gly Asn Pro Met Lys Arg Gly Ala Gln Val Thr
755 760 765

Phe Tyr Leu Ile Leu Ser Thr Ser Gly Ile Ser Ile Glu Thr Thr
770 775 780

Glu Leu Glu Val Glu Leu Leu Leu Ala Thr Ile Ser Glu Gln Glu
785 790 795

Leu His Pro Val Ser Ala Arg Ala Arg Val Phe Ile Glu Leu Pro
800 805 810

Leu Ser Ile Ala Gly Met Ala Ile Pro Gln Gln Leu Phe Phe Ser
815 820 825

Gly Val Val Arg Gly Glu Arg Ala Met Gln Ser Glu Arg Asp Val
830 835 840

Gly Ser Lys Val Lys Tyr Glu Val Thr Val Ser Asn Gln Gly Gln
845 850 855

Ser Leu Arg Thr Leu Gly Ser Ala Phe Leu Asn Ile Met Trp Pro
860 865 870

His Glu Ile Ala Asn Gly Lys Trp Leu Leu Tyr Pro Met Gln Val
875 880 885

Glu Leu Glu Gly Gly Gln Gly Pro Gly Gln Lys Gly Leu Cys Ser
890 895 900

Pro Arg Pro Asn Ile Leu His Leu Asp Val Asp Ser Arg Asp Arg
905 910 915

Arg Arg Arg Glu Leu Glu Pro Pro Glu Gln Gln Glu Pro Gly Glu
920 925 930

Arg Gln Glu Pro Ser Met Ser Trp Trp Pro Val Ser Ser Ala Glu
935 940 945

Lys Lys Lys Asn Ile Thr Leu Asp Cys Ala Arg Gly Thr Ala Asn
950 955 960

```
Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala
                965                 970                 975

Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu
                980                 985                 990

Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn
                995                 1000                1005

Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala
                1010                1015                1020

Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val
                1025                1030                1035

Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu
                1040                1045                1050

Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys
                1055                1060                1065

Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro
                1070                1075                1080

Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe
                1085                1090                1095

Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser
                1100                1105                1110

Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp
                1115                1120                1125

Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr
                1130                1135                1140

Ala
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<210> 438
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 438
ggctgacacc gcagtgctct tcag 24

<210> 439
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 439
gctgctgggg actgcaatgt agct 24

<210> 440
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 440
catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441
<211> 1964
<212> DNA
<213> Homo sapiens

<400> 441
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agcagctcca gaaagcagcg agttggcaga gcagggctgc atttccagca 100

ggagctgcga gcacagtgct ggctcacaac aagatgctca aggtgtcagc 150

cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctcgcagctg 200

ccgcggcggt ggctgcagcc gggggcggt cggacggcgg taattttctg 250

gatgataaac aatggctcac cacaatctct cagtatgaca aggaagtcgg 300

acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350

ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400

tgcttaaaga tgaaatgtag tcgccataaa gtatgcattg ctcaagattc 450

tcagactgca gtctgcatta gtcaccggag gcttacacac aggatgaaag 500

aagcaggagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550

aagcagtgcc cagtggtcta tcccagccct gtttgtggtt cagatggtca 600

tacctactct tttcagtgca aactagaata tcaggcatgt gtcttaggaa 650

aacagatctc agtcaaatgt gaaggacatt gcccatgtcc ttcagataag 700

cccaccagta caagcagaaa tgttaagaga gcatgcagtg acctggagtt 750

cagggaagtg gcaaacagat tgcgggactg gttcaaggcc cttcatgaaa 800

gtggaagtca aaacaagaag acaaaaacat tgctgaggcc tgagagaagc 850

agattcgata ccagcatctt gccaatttgc aaggactcac ttggctggat 900

gtttaacaga cttgatacaa actatgacct gctattggac cagtcagagc 950 tcagaagcat ttaccttgat aagaatgaac agtgtaccaa ggcattcttc 1000

aattcttgtg acacatacaa ggacagttta atatctaata atgagtggtg 1050

ctactgcttc cagagacagc aagacccacc ttgccagact gagctcagca 1100

atattcagaa gcggcaaggg gtaaagaagc tcctaggaca gtatatcccc 1150

ctgtgtgatg aagatggtta ctacaagcca acacaatgtc atggcagtgt 1200

tggacagtgc tggtgtgttg acagatatgg aaatgaagtc atgggatcca 1250

gaataaatgg tgttgcagat tgtgctatag attttgagat ctccggagat 1300

tttgctagtg gcgattttca tgaatggact gatgatgagg atgatgaaga 1350

cgatattatg aatgatgaag atgaaattga agatgatgat gaagatgaag 1400

gggatgatga tgatggtggt gatgaccatg atgtatacat ttgattgatg 1450

acagttgaaa tcaataaatt ctacatttct aatatttaca aaaatgatag 1500

cctatttaaa attatcttct tccccaataa caaaatgatt ctaaacctca 1550

catatatttt gtataattat ttgaaaaatt gcagctaaag ttatagaact 1600

ttatgtttaa ataagaatca tttgctttga gtttttatat tccttacaca 1650

aaaagaaaat acatatgcag tctagtcaga caaaataaag ttttgaagtg 1700

ctactataat aaatttttca cgagaacaaa ctttgtaaat cttccataag 1750

caaaatgaca gctagtgctt gggatcgtac atgttaattt tttgaaagat 1800

aattctaagt gaaatttaaa ataaataaat ttttaatgac ctgggtctta 1850

aggatttagg aaaaatatgc atgctttaat tgcatttcca aagtagcatc 1900

ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950

aaaaaaaaaa aaaa 1964

<210> 442
<211> 436
<212> PRT
<213> Homo sapiens

<400> 442

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Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Trp
  1               5                  10                  15

Cys Ser Gln Ser Leu Ala Ala Ala Ala Ala Val Ala Ala Ala Gly
                 20                  25                  30

Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu
                 35                  40                  45

Thr Thr Ile Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys
```

```
                50                       55                       60

Phe Arg Asp Glu Val Glu Asp Asp Tyr Phe Arg Thr Trp Ser Pro
                65                       70                       75

Gly Lys Pro Phe Asp Gln Ala Leu Asp Pro Ala Lys Asp Pro Cys
                80                       85                       90

Leu Lys Met Lys Cys Ser Arg His Lys Val Cys Ile Ala Gln Asp
                95                       100                      105

Ser Gln Thr Ala Val Cys Ile Ser His Arg Arg Leu Thr His Arg
                110                      115                      120

Met Lys Glu Ala Gly Val Asp His Arg Gln Trp Arg Gly Pro Ile
                125                      130                      135

Leu Ser Thr Cys Lys Gln Cys Pro Val Val Tyr Pro Ser Pro Val
                140                      145                      150

Cys Gly Ser Asp Gly His Thr Tyr Ser Phe Gln Cys Lys Leu Glu
                155                      160                      165

Tyr Gln Ala Cys Val Leu Gly Lys Gln Ile Ser Val Lys Cys Glu
                170                      175                      180

Gly His Cys Pro Cys Pro Ser Asp Lys Pro Thr Ser Thr Ser Arg
                185                      190                      195

Asn Val Lys Arg Ala Cys Ser Asp Leu Glu Phe Arg Glu Val Ala
                200                      205                      210

Asn Arg Leu Arg Asp Trp Phe Lys Ala Leu His Glu Ser Gly Ser
                215                      220                      225

Gln Asn Lys Lys Thr Lys Thr Leu Leu Arg Pro Glu Arg Ser Arg
                230                      235                      240

Phe Asp Thr Ser Ile Leu Pro Ile Cys Lys Asp Ser Leu Gly Trp
                245                      250                      255

Met Phe Asn Arg Leu Asp Thr Asn Tyr Asp Leu Leu Leu Asp Gln
                260                      265                      270

Ser Glu Leu Arg Ser Ile Tyr Leu Asp Lys Asn Glu Gln Cys Thr
                275                      280                      285

Lys Ala Phe Phe Asn Ser Cys Asp Thr Tyr Lys Asp Ser Leu Ile
                290                      295                      300

Ser Asn Asn Glu Trp Cys Tyr Cys Phe Gln Arg Gln Gln Asp Pro
                305                      310                      315

Pro Cys Gln Thr Glu Leu Ser Asn Ile Gln Lys Arg Gln Gly Val
                320                      325                      330

Lys Lys Leu Leu Gly Gln Tyr Ile Pro Leu Cys Asp Glu Asp Gly
                335                      340                      345
```

```
Tyr Tyr Lys Pro Thr Gln Cys His Gly Ser Val Gly Gln Cys Trp
                350                 355                 360

Cys Val Asp Arg Tyr Gly Asn Glu Val Met Gly Ser Arg Ile Asn
                365                 370                 375

Gly Val Ala Asp Cys Ala Ile Asp Phe Glu Ile Ser Gly Asp Phe
                380                 385                 390

Ala Ser Gly Asp Phe His Glu Trp Thr Asp Asp Glu Asp Asp Glu
                395                 400                 405

Asp Asp Ile Met Asn Asp Glu Asp Glu Ile Glu Asp Asp Asp Glu
                410                 415                 420

Asp Glu Gly Asp Asp Asp Asp Gly Gly Asp Asp His Asp Val Tyr
                425                 430                 435

Ile


<210> 443
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 443
 cagcaatatt cagaagcggc aaggg 25

<210> 444
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 444
 catcatggtc atcaccacca tcatcatc 28

<210> 445
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 445
 ggttactaca agccaacaca atgtcatggc agtgttggac agtgctgg 48

<210> 446
<211> 3617
<212> DNA
<213> Homo sapiens
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<400> 446
cagactccag atttccctgt caaccacgag gagtccagag aggaaacgcg 50

gagcggagac aacagtacct gacgcctctt tcagcccggg atcgccccag 100

cagggatggg cgacaagatc tggctgccct tccccgtgct ccttctggcc 150

gctctgcctc cggtgctgct gcctggggcg gccggcttca caccttccct 200

cgatagcgac ttcaccttta cccttcccgc cggccagaag gagtgcttct 250

accagcccat gcccctgaag gcctcgctgg agatcgagta ccaagtttta 300

gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa 350

aaccttagtt tttgaacaaa gaaaatcaga tggagttcac actgtagaga 400

ctgaagttgg tgattacatg ttctgctttg acaatacatt cagcaccatt 450

tctgagaagg tgattttctt tgaattaatc ctggataata tgggagaaca 500

ggcacaagaa caagaagatt ggaagaaata tattactggc acagatatat 550

tggatatgaa actggaagac atcctggaat ccatcaacag catcaagtcc 600

agactaagca aaagtgggca catacaaatt ctgcttagag catttgaagc 650

tcgtgatcga aacatacaag aaagcaactt tgatagagtc aatttctggt 700

ctatggttaa tttagtggtc atggtggtgg tgtcagccat tcaagtttat 750

atgctgaaga gtctgtttga agataagagg aaaagtagaa cttaaaactc 800

caaactagag tacgtaacat tgaaaaatga ggcataaaaa tgcaataaac 850

tgttacagtc aagaccatta atggtcttct ccaaaatatt ttgagatata 900

aaagtaggaa acaggtataa ttttaatgtg aaaattaagt cttcactttc 950

tgtgcaagta atcctgctga tccagttgta cttaagtgtg taacaggaat 1000

attttgcaga atataggttt aactgaatga agccatatta ataactgcat 1050

tttcctaact ttgaaaaatt ttgcaaatgt cttaggtgat ttaaataaat 1100

gagtattggg cctaattgca acaccagtct gtttttaaca ggttctatta 1150

cccagaactt ttttgtaaat gcggcagtta caaattaact gtggaagttt 1200

tcagttttaa gttataaatc acctgagaat tacctaatga tggattgaat 1250

aaatctttag actacaaaag cccaactttt ctctatttac atatgcatct 1300

ctcctataat gtaaatagaa taatagcttt gaaatacaat taggtttttg 1350

agatttttat aaccaaatac atttcagtgt aacatattag cagaaagcat 1400

tagtctttgt actttgctta cattcccaaa agctgacatt ttcacgattc 1450 ttaaaaacac aaagttacac ttactaaaat taggacatgt tttctctttg 1500

aaatgaagaa tatagtttaa aagcttcctc ctccataggg acacattttc 1550

tctaaccctt aactaaagtg taggatttta aaattaaatg tgaggtaaaa 1600

taagtttatt tttaatagta tctgtcaagt taatatctgt caacagttaa 1650

taatcatgtt atgttaattt taacatgatt gctgacttgg ataattcatt 1700

attaccagca gttatgaagg aaatattgct aaaatgatct gggcctacca 1750

taaataaata tctccttttc tgagctctaa gaattatcag aaaacaggaa 1800

agaatttaga aaaacttgag aaaacctaat ccaaaataaa attcacttaa 1850

gtagaactat aaataaatat ctagaatctg actggctcat catgacatcc 1900

tactcataac ataaatcaaa ggagatgatt aatttccagt tagctggaag 1950

aaactttggc tgtaggtttt tattttctac aagaattctg gtttgaatta 2000

tttttgtaag caggtacatt ttataaaatg taagccctac tgtaaggttt 2050

agcactgggt gtacatattt attaaaaatt tttattataa caacttttat 2100

taaaatggcc tttctgaaca ctttatttat tgatgttgaa gtaaggatta 2150

gaaacataga ctcccaagtt ttaaacacct aaatgtgaat aacccatata 2200

tacaacaaag tttctgccat ctagcttttt gaagtctatg gggtcttac 2250

tcaagtacta gtaatttaac ttcatcatga atgaactata atttttaagt 2300

tatgcccatt tataacgttg tttatgacta cattgtgagt tagaaacaaa 2350

cttaaaattt ggggtataga acccctcaac aggttagtaa tgctggaatt 2400

cttgatgagc aataatgata accagagagt gatttcattt acactcatag 2450

tagtataaaa agagatacat ttccctctta ggcccctggg agaagagcag 2500

cttagatttc cctactggca aggtttttaa aaatgaggta aatgccgtat 2550

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ataccсctcc cttttgcgct gttaaatttg caatgagaag caaatttaca 2700

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tataaaactg tgattaagaa ttctacctct cctgtatggc tgttactgta 2800

ctgtactctc tgactcctta cctaacaatg aatttgttac ataatcttct 2850

acatgtatga tttgtgccac tgatcttaaa cctatgattc agtaacttct 2900

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taccatataa aaacgataat tgctttattt ggaaaagaat ttaggaatac 2950

taaggacaat tatttttata gacaaagtaa aaagacagat atttaagagg 3000

cataaccaaa aaagcaaaac ttgtaaacag agtaaaaatc tttaatattt 3050

ctaaagacat actgtttatc tgcttcatat gcttttttta atttcactat 3100

tccatttcta aattaaagtt atgctaaatt gagtaagctg tttatcactt 3150

aacagctcat tttgtctttt tcaatataca aattttaaaa atactacaat 3200

atttaactaa ggcccaaccg atttccataa tgtagcagtt accgtgttca 3250

cctcacacta aggcctagag tttgctctga tatgcatttg gatgattaat 3300

gttatgctgt tctttcatgt gaatgtcaag acatggaggg tgtttgtaat 3350

tttatggtaa aattaatcct tcttacacat aatggtgtct taaaattgac 3400

aaaaaatgag cacttacaat tgtatgtctc ctcaaatgaa gattctttat 3450

gtgaaatttt aaaagacatt gattccgcat gtaaggattt ttcatctgaa 3500

gtacaataat gcacaatcag tgttgctcaa actgctttat acttataaac 3550

agccatctta aataagcaac gtattgtgag tactgatatg tatataataa 3600

aaattatcaa aggaaaa 3617

<210> 447
<211> 229
<212> PRT
<213> Homo sapiens

<400> 447
 Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala
   1               5                  10                  15

 Ala Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro
                  20                  25                  30

 Ser Leu Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys
                  35                  40                  45

 Glu Cys Phe Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile
                  50                  55                  60

 Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His
                  65                  70                  75

 Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys
                  80                  85                  90

 Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met
                  95                 100                 105

 Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile
```

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                110                 115                 120

Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu
                125                 130                 135

Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp
                140                 145                 150

Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser
                155                 160                 165

Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe
                170                 175                 180

Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val
                185                 190                 195

Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser
                200                 205                 210

Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg
                215                 220                 225

Lys Ser Arg Thr
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<210> 448
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 449
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 449
gtcttccagt ttcatatcca ata 23

<210> 450
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 450
ccagaaggag cacggggaag ggcagccaga tcttgtcgcc cat 43

<210> 451
<211> 859
<212> DNA
<213> Homo sapiens

<400> 451
ccatccctga gatcttttta taaaaaaccc agtctttgct gaccagacaa 50

agcataccag atctcaccag agagtcgcag acactatgct gcctcccatg 100

gccctgccca gtgtgtcctg gatgctgctt tcctgcctca ttctcctgtg 150

tcaggttcaa ggtgaagaaa cccagaagga actgccctct ccacggatca 200

gctgtcccaa aggctccaag gcctatggct ccccctgcta tgccttgttt 250

ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300

ctctggaaaa ctggtgtctg tgctcagtgg ggctgaggga tccttcgtgt 350

cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400

ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450

gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500

ccatcttaaa ccctggccac tgtgggagcc tgtcaagaag cacaggattt 550

ctgaagtgga aagattataa ctgtgatgca aagttaccct atgtctgcaa 600

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gctcatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700

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ttcctttttc ttcaccttca tttcaggctt ttctctgtct tccatgtctt 800

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aaaaaaaaa 859

<210> 452
<211> 175
<212> PRT
<213> Homo sapiens

<400> 452
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Ser Cys Leu Ile Leu Leu Cys Gln Val Gln Gly Glu Glu Thr Gln
20 25 30

Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys
35 40 45

Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser

50 55 60

Trp Met Asp Ala Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Lys
65 70 75

Leu Val Ser Val Leu Ser Gly Ala Glu Gly Ser Phe Val Ser Ser
80 85 90

Leu Val Arg Ser Ile Ser Asn Ser Tyr Ser Tyr Ile Trp Ile Gly
95 100 105

Leu His Asp Pro Thr Gln Gly Ser Glu Pro Asp Gly Asp Gly Trp
110 115 120

Glu Trp Ser Ser Thr Asp Val Met Asn Tyr Phe Ala Trp Glu Lys
125 130 135

Asn Pro Ser Thr Ile Leu Asn Pro Gly His Cys Gly Ser Leu Ser
140 145 150

Arg Ser Thr Gly Phe Leu Lys Trp Lys Asp Tyr Asn Cys Asp Ala
155 160 165

Lys Leu Pro Tyr Val Cys Lys Phe Lys Asp
170 175

<210> 453
<211> 550
<212> DNA
<213> Homo sapiens

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tgcgctgcta cgtctgtccg gagcccacag gagtgtcgga ctgtgtcacc 200

atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250

ccgggagata gtgtacccct tccaggggga ctccacggtg accaagtcct 300

gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350

cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgcccgc 400

tctgaacagc ctccactgcg gggccctcac gctcctccca ctcttgagcc 450

tccgactgta gagtccccgc ccacccccat ggccctatgc ggcccagccc 500

cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaa aaaaaaaaaa 550

<210> 454
<211> 125
<212> PRT
<213> Homo sapiens

<400> 454

Met Arg Gly Thr Arg Leu Ala Leu Leu Ala Leu Val Leu Ala Ala
1   5   10   15

Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu
                20   25   30

Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr
                35   40   45

Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val
                50   55   60

Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser
                65   70   75

Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro
                80   85   90

Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro
                95   100   105

Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu
                110   115   120

Leu Ser Leu Arg Leu
                125

<210> 455
<211> 1518
<212> DNA
<213> Homo sapiens

<400> 455

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gcgcagcggg agctacccgg gtctttgtcg cgatggtagc ggcggctctc 200

ggcggccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250

ttccaacgct atcaagaacc tgcccccacc gctgggcggc gctgcggggc 300

acccaggctc tgcagtcagc gccgcgccgg gaatcctgta cccgggcggg 350

aataagtacc agaccattga caactaccag ccgtacccgt gcgcagagga 400

cgaggagtgc ggcactgatg agtactgcgc tagtcccacc cgcggagggg 450

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atgcgtcacg ctatgtgctg ccccgggaat tactgcaaaa atggaatatg 550

tgtgtcttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600 ctgaaagctt tggtaatgat catagcacct tggatgggta ttccagaaga 650

accaccttgt cttcaaaaat gtatcacacc aaaggacaag aaggttctgt 700

ttgtctccgg tcatcagact gtgcctcagg attgtgttgt gctagacact 750

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ctgtggagaa ggtctgtctt gccggataca gaaagatcac catcaagcca 900

gtaattcttc taggcttcac acttgtcaga gacactaaac cagctatcca 950

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ccttcatcaa ctcaatccta aggatataca agttctgtgg tttcagttaa 1050

gcattccaat aacaccttcc aaaaacctgg agtgtaagag ctttgtttct 1100

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tgattgttat cttgactgac aaatattcta tattgaactg aagtaaatca 1300

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gagtctagaa cgcaaggatc tcttggaatg acaaatgata ggtacctaaa 1400

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catttaaaaa aaaaaaaa 1518

<210> 456
<211> 266
<212> PRT
<213> Homo sapiens

<400> 456
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Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala
  1               5                  10                  15

Met Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser
                 20                  25                  30

Ala Thr Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu
                 35                  40                  45

Pro Pro Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val
                 50                  55                  60

Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln
                 65                  70                  75
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Thr Ile Asp Asn Tyr Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu
80 85 90

Cys Gly Thr Asp Glu Tyr Cys Ala Ser Pro Thr Arg Gly Gly Asp
95 100 105

Ala Gly Val Gln Ile Cys Leu Ala Cys Arg Lys Arg Arg Lys Arg
110 115 120

Cys Met Arg His Ala Met Cys Cys Pro Gly Asn Tyr Cys Lys Asn
125 130 135

Gly Ile Cys Val Ser Ser Asp Gln Asn His Phe Arg Gly Glu Ile
140 145 150

Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn Asp His Ser Thr Leu
155 160 165

Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser Lys Met Tyr His
170 175 180

Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser Ser Asp Cys
185 190 195

Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys Ile Cys
200 205 210

Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg Arg
215 220 225

Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly
230 235 240

Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser
245 250 255

Asn Ser Ser Arg Leu His Thr Cys Gln Arg His
260 265

<210> 457
<211> 638
<212> DNA
<213> Homo sapiens

<220>
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509, 556
<223> unknown base

<400> 457
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catttttttt tctttctcct tcnggagtcc ttntgagang atggttttgg 150

gcgcagcggg agctaacccg gttttttgtn gcgatggtag cggcggtttt 200

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 aataagtacc agaccattga caattaccag ccgtacccgt gcgcagagga 400

 cgaggagtgc ggcactgatg agtactgcgc tagtcccacc cgcggagggg 450

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 atgcgtcang ctatgtgctg ccccgggaat tactgcaaaa atggaatatg 550

 tgtgtnttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600

 ctgaaagctt tggtaatgat catagcacct tggatggg 638

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<211> 4040
<212> DNA
<213> Homo sapiens

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 gggtttgagg atgggggagt agctacagga agcgaccccg cgatggcaag 200

 gtatattttt gtggaatgaa aaggaagtat tagaaatgag ctgaagacca 250

 ttcacagatt aatatttttg gggacagatt tgtgatgctt gattcaccct 300

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 accagcagtg aatcttaatg ttcacttaaa tcagaacttg cataagaaag 400

 agaatgggag tctggttaaa taaagatgac tatatcagag acttgaaaag 450

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 gaaataagac aagctttcaa gaaattggca ttgaagttac atcctgataa 600

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 ggagaaaagg gacttgagga taatcaaggt ggccagtatg aaagctggaa 750

 ctattatcgt tatgattttg gtatttatga tgatgatcct gaaatcataa 800

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<212> PRT
<213> Homo sapiens

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                 20                  25                  30

Gly Thr Asp Gln Asp Phe Tyr Ser Leu Leu Gly Val Ser Lys Thr
                 35                  40                  45

Ala Ser Ser Arg Glu Ile Arg Gln Ala Phe Lys Lys Leu Ala Leu
                 50                  55                  60

Lys Leu His Pro Asp Lys Asn Pro Asn Asn Pro Asn Ala His Gly
                 65                  70                  75

Asp Phe Leu Lys Ile Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu
                 80                  85                  90

Asp Leu Arg Lys Lys Tyr Asp Lys Tyr Gly Glu Lys Gly Leu Glu
                 95                 100                 105

Asp Asn Gln Gly Gly Gln Tyr Glu Ser Trp Asn Tyr Tyr Arg Tyr
                110                 115                 120

Asp Phe Gly Ile Tyr Asp Asp Asp Pro Glu Ile Ile Thr Leu Glu
                125                 130                 135

Arg Arg Glu Phe Asp Ala Ala Val Asn Ser Gly Glu Leu Trp Phe
                140                 145                 150

Val Asn Phe Tyr Ser Pro Gly Cys Ser His Cys His Asp Leu Ala
                155                 160                 165

Pro Thr Trp Arg Asp Phe Ala Lys Glu Val Asp Gly Leu Leu Arg
                170                 175                 180

Ile Gly Ala Val Asn Cys Gly Asp Asp Arg Met Leu Cys Arg Met
                185                 190                 195

Lys Gly Val Asn Ser Tyr Pro Ser Leu Phe Ile Phe Arg Ser Gly
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Met Ala Pro Val Lys Tyr His Gly Asp Arg Ser Lys Glu Ser Leu
                215                 220                 225

Val Ser Phe Ala Met Gln His Val Arg Ser Thr Val Thr Glu Leu
                230                 235                 240

Trp Thr Gly Asn Phe Val Asn Ser Ile Gln Thr Ala Phe Ala Ala
                245                 250                 255

Gly Ile Gly Trp Leu Ile Thr Phe Cys Ser Lys Gly Gly Asp Cys
                260                 265                 270

Leu Thr Ser Gln Thr Arg Leu Arg Leu Ser Gly Met Leu Phe Leu
                275                 280                 285

Asn Ser Leu Asp Ala Lys Glu Ile Tyr Leu Glu Val Ile His Asn
                290                 295                 300

Leu Pro Asp Phe Glu Leu Leu Ser Ala Asn Thr Leu Glu Asp Arg
                305                 310                 315

Leu Ala His His Arg Trp Leu Leu Phe Phe His Phe Gly Lys Asn
                320                 325                 330

Glu Asn Ser Asn Asp Pro Glu Leu Lys Lys Leu Lys Thr Leu Leu
                335                 340                 345

Lys Asn Asp His Ile Gln Val Gly Arg Phe Asp Cys Ser Ser Ala
                350                 355                 360

Pro Asp Ile Cys Ser Asn Leu Tyr Val Phe Gln Pro Ser Leu Ala
                365                 370                 375

Val Phe Lys Gly Gln Gly Thr Lys Glu Tyr Glu Ile His His Gly
                380                 385                 390

Lys Lys Ile Leu Tyr Asp Ile Leu Ala Phe Ala Lys Glu Ser Val
                395                 400                 405

Asn Ser His Val Thr Thr Leu Gly Pro Gln Asn Phe Pro Ala Asn
                410                 415                 420

Asp Lys Glu Pro Trp Leu Val Asp Phe Phe Ala Pro Trp Cys Pro
                425                 430                 435

Pro Cys Arg Ala Leu Leu Pro Glu Leu Arg Arg Ala Ser Asn Leu
                440                 445                 450

Leu Tyr Gly Gln Leu Lys Phe Gly Thr Leu Asp Cys Thr Val His
                455                 460                 465

Glu Gly Leu Cys Asn Met Tyr Asn Ile Gln Ala Tyr Pro Thr Thr
                470                 475                 480

Val Val Phe Asn Gln Ser Asn Ile His Glu Tyr Glu Gly His His
                485                 490                 495
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Ser Ala Glu Gln Ile Leu Glu Phe Ile Glu Asp Leu Met Asn Pro
                500                 505                 510

Ser Val Val Ser Leu Thr Pro Thr Thr Phe Asn Glu Leu Val Thr
                515                 520                 525

Gln Arg Lys His Asn Glu Val Trp Met Val Asp Phe Tyr Ser Pro
                530                 535                 540

Trp Cys His Pro Cys Gln Val Leu Met Pro Glu Trp Lys Arg Met
                545                 550                 555

Ala Arg Thr Leu Thr Gly Leu Ile Asn Val Gly Ser Ile Asp Cys
                560                 565                 570

Gln Gln Tyr His Ser Phe Cys Ala Gln Glu Asn Val Gln Arg Tyr
                575                 580                 585

Pro Glu Ile Arg Phe Phe Pro Pro Lys Ser Asn Lys Ala Tyr Gln
                590                 595                 600

Tyr His Ser Tyr Asn Gly Trp Asn Arg Asp Ala Tyr Ser Leu Arg
                605                 610                 615

Ile Trp Gly Leu Gly Phe Leu Pro Gln Val Ser Thr Asp Leu Thr
                620                 625                 630

Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys Asn His Trp
                635                 640                 645

Val Ile Asp Phe Tyr Ala Pro Trp Cys Gly Pro Cys Gln Asn Phe
                650                 655                 660

Ala Pro Glu Phe Glu Leu Leu Ala Arg Met Ile Lys Gly Lys Val
                665                 670                 675

Lys Ala Gly Lys Val Asp Cys Gln Ala Tyr Ala Gln Thr Cys Gln
                680                 685                 690

Lys Ala Gly Ile Arg Ala Tyr Pro Thr Val Lys Phe Tyr Phe Tyr
                695                 700                 705

Glu Arg Ala Lys Arg Asn Phe Gln Glu Glu Gln Ile Asn Thr Arg
                710                 715                 720

Asp Ala Lys Ala Ile Ala Ala Leu Ile Ser Glu Lys Leu Glu Thr
                725                 730                 735

Leu Arg Asn Gln Gly Lys Arg Asn Lys Asp Glu Leu
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<213> Artificial Sequence

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<400> 460
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<210> 461
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 461
gatcagccag ccaataccag cagc 24

<210> 462
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 462
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<210> 463
<211> 1818
<212> DNA
<213> Homo sapiens

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caccatcatc tactcctact tggagtcgtt ggtgaagttt ttcattcctc 150

agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 200

catggaatag gcaggcagac tacttatgaa tttgcaaaac gacagagcat 250

attggttctg tgggatatta ataagcgcgg tgtggaggaa actgcagctg 300

agtgccgaaa actaggcgtc actgcgcatg cgtatgtggt agactgcagc 350

aacagagaag agatctatcg ctctctaaat caggtgaaga aagaagtggg 400

tgatgtaaca atcgtggtga ataatgctgg gacagtatat ccagccgatc 450

ttctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 500

ctaggacatt tttggatcac aaaagcactt cttccatcga tgatggagag 550

aaatcatggc cacatcgtca cagtggcttc agtgtgcggc cacgaaggga 600

ttccttacct catcccatat tgttccagca aatttgccgc tgttggcttt 650

cacagaggtc tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa 700 aacctcatgt ctctgcccag tttttgtgaa tactgggttc accaaaaatc 750

caagcacaag attatggcct gtattggaga cagatgaagt cgtaagaagt 800

ctgatagatg gaatacttac caataagaaa atgatttttg ttccatcgta 850

tatcaatatc tttctgagac tacagaagtt tcttcctgaa cgcgcctcag 900

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gtagtttttc ataggtctgt ttttcctttc atgcctctta aaaacttctg 1200

tgcttacata aacatactta aaaggttttc tttaagatat tttatttttc 1250

catttaaagg tggacaaaag ctacctccct aaaagtaaat acaaagagaa 1300

cttatttaca cagggaaggt ttaagactgt tcaagtagca ttccaatctg 1350

tagccatgcc acagaatatc aacaagaaca cagaatgagt gcacagctaa 1400

gagatcaagt ttcagcaggc agctttatct caacctggac atattttaag 1450

attcagcatt tgaaagattt ccctagcctc ttcctttttc attagcccaa 1500

aacggtgcaa ctctattctg gactttatta cttgattctg tcttctgtat 1550

aactctgaag tccaccaaaa gtggaccctc tatatttcct ccctttttat 1600

agtcttataa gatacattat gaaaggtgac cgactctatt ttaaatctca 1650

gaattttaag ttctagcccc atgataacct ttttctttgt aatttatgct 1700

ttcatatatc cttggtccca gagatgttta gacaatttta ggctcaaaaa 1750

ttaaagctaa cacaggaaaa ggaactgtac tggctattac ataagaaaca 1800

atggacccaa gagaagaa 1818

<210> 464
<211> 300
<212> PRT
<213> Homo sapiens

<400> 464
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Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Leu Ile Thr Ile Ile
 1               5                  10                  15

Tyr Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg
            20                  25                  30
```

Arg Lys Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly
35 40 45

His Gly Ile Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln
50 55 60

Ser Ile Leu Val Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu
65 70 75

Thr Ala Ala Glu Cys Arg Lys Leu Gly Val Thr Ala His Ala Tyr
80 85 90

Val Val Asp Cys Ser Asn Arg Glu Glu Ile Tyr Arg Ser Leu Asn
95 100 105

Gln Val Lys Lys Glu Val Gly Asp Val Thr Ile Val Val Asn Asn
110 115 120

Ala Gly Thr Val Tyr Pro Ala Asp Leu Leu Ser Thr Lys Asp Glu
125 130 135

Glu Ile Thr Lys Thr Phe Glu Val Asn Ile Leu Gly His Phe Trp
140 145 150

Ile Thr Lys Ala Leu Leu Pro Ser Met Met Glu Arg Asn His Gly
155 160 165

His Ile Val Thr Val Ala Ser Val Cys Gly His Glu Gly Ile Pro
170 175 180

Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe
185 190 195

His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys Thr Gly
200 205 210

Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly Phe
215 220 225

Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp
230 235 240

Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys
245 250 255

Met Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln
260 265 270

Lys Phe Leu Pro Glu Arg Ala Ser Ala Ile Leu Asn Arg Met Gln
275 280 285

Asn Ile Gln Phe Glu Ala Val Val Gly His Lys Ile Lys Met Lys
290 295 300

<210> 465
<211> 1547
<212> DNA
<213> Homo sapiens

<400> 465
cggcggcggc tgcgggcgcg aggtgagggg cgcgaggtga ggggcgcgag 50

gttcccagca ggatgccccg gctctgcagg aagctgaagt gagaggcccg 100

gagagggccc agcccgcccg gggcaggatg accaaggccc ggctgttccg 150

gctgtggctg gtgctggggt cggtgttcat gatcctgctg atcatcgtgt 200

actgggacag cgcaggcgcc gcgcacttct acttgcacac gtccttctct 250

aggccgcaca cggggccgcc gctgcccacg cccgggccgg acagggacag 300

ggagctcacg gccgactccg atgtcgacga gtttctggac aagtttctca 350

gtgctggcgt gaagcagagc gaccttccca gaaaggagac ggagcagccg 400

cctgcgccgg ggagcatgga ggagagcgtg agaggctacg actggtcccc 450

gcgcgacgcc cggcgcagcc cagaccaggg ccggcagcag gcggagcgga 500

ggagcgtgct gcggggcttc tgcgccaact ccagcctggc cttccccacc 550

aaggagcgcg cattcgacga catccccaac tcggagctga gccacctgat 600

cgtggacgac cggcacgggg ccatctactg ctacgtgccc aaggtggcct 650

gcaccaactg gaagcgcgtg atgatcgtgc tgagcggaag cctgctgcac 700

cgcggtgcgc cctaccgcga cccgctgcgc atcccgcgcg agcacgtgca 750

caacgccagc gcgcacctga ccttcaacaa gttctggcgc cgctacggga 800

agctctcccg ccacctcatg aaggtcaagc tcaagaagta caccaagttc 850

ctcttcgtgc gcgacccctt cgtgcgcctg atctccgcct tccgcagcaa 900

gttcgagctg gagaacgagg agttctaccg caagttcgcc gtgcccatgc 950

tgcggctgta cgccaaccac accagcctgc ccgcctcggc gcgcgaggcc 1000

ttccgcgctg gcctcaaggt gtccttcgcc aacttcatcc agtacctgct 1050

ggacccgcac acggagaagc tggcgccctt caacgagcac tggcggcagg 1100

tgtaccgcct ctgccacccg tgccagatcg actacgactt cgtggggaag 1150

ctggagactc tggacgagga cgccgcgcag ctgctgcagc tactccaggt 1200

ggaccggcag ctccgcttcc ccccgagcta ccggaacagg accgccagca 1250

gctgggagga ggactggttc gccaagatcc ccctggcctg gaggcagcag 1300

ctgtataaac tctacgaggc cgactttgtt ctcttcggct accccaagcc 1350

cgaaaacctc ctccgagact gaaagctttc gcgttgcttt ttctcgcgtg 1400

cctggaacct gacgcacgcg cactccagtt tttttatgac ctacgatttt 1450

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gcaatctggg cttcttgttc actccactgc ctctatccat tgagtactgt 1500

atcgatattg ttttttaaga ttaatatatt tcaggtattt aatacga 1547
```

<210> 466
<211> 414
<212> PRT
<213> Homo sapiens

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<400> 466
Met Thr Lys Ala Arg Leu Phe Arg Leu Trp Leu Val Leu Gly Ser
 1               5                  10                  15

Val Phe Met Ile Leu Leu Ile Ile Val Tyr Trp Asp Ser Ala Gly
                20                  25                  30

Ala Ala His Phe Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr
                35                  40                  45

Gly Pro Pro Leu Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu
                50                  55                  60

Thr Ala Asp Ser Asp Val Asp Glu Phe Leu Asp Lys Phe Leu Ser
                65                  70                  75

Ala Gly Val Lys Gln Ser Asp Leu Pro Arg Lys Glu Thr Glu Gln
                80                  85                  90

Pro Pro Ala Pro Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp
                95                 100                 105

Trp Ser Pro Arg Asp Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln
               110                 115                 120

Gln Ala Glu Arg Arg Ser Val Leu Arg Gly Phe Cys Ala Asn Ser
               125                 130                 135

Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro
               140                 145                 150

Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg His Gly Ala
               155                 160                 165

Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp Lys Arg
               170                 175                 180

Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala Pro
               185                 190                 195

Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala
               200                 205                 210

Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys
               215                 220                 225

Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys
               230                 235                 240
```

```
Phe Leu Phe Val Arg Asp Pro Phe Val Arg Leu Ile Ser Ala Phe
                245                 250                 255

Arg Ser Lys Phe Glu Leu Glu Asn Glu Glu Phe Tyr Arg Lys Phe
                260                 265                 270

Ala Val Pro Met Leu Arg Leu Tyr Ala Asn His Thr Ser Leu Pro
                275                 280                 285

Ala Ser Ala Arg Glu Ala Phe Arg Ala Gly Leu Lys Val Ser Phe
                290                 295                 300

Ala Asn Phe Ile Gln Tyr Leu Leu Asp Pro His Thr Glu Lys Leu
                305                 310                 315

Ala Pro Phe Asn Glu His Trp Arg Gln Val Tyr Arg Leu Cys His
                320                 325                 330

Pro Cys Gln Ile Asp Tyr Asp Phe Val Gly Lys Leu Glu Thr Leu
                335                 340                 345

Asp Glu Asp Ala Ala Gln Leu Leu Gln Leu Leu Gln Val Asp Arg
                350                 355                 360

Gln Leu Arg Phe Pro Pro Ser Tyr Arg Asn Arg Thr Ala Ser Ser
                365                 370                 375

Trp Glu Glu Asp Trp Phe Ala Lys Ile Pro Leu Ala Trp Arg Gln
                380                 385                 390

Gln Leu Tyr Lys Leu Tyr Glu Ala Asp Phe Val Leu Phe Gly Tyr
                395                 400                 405

Pro Lys Pro Glu Asn Leu Leu Arg Asp
                410
```

<210> 467
<211> 1071
<212> DNA
<213> Homo sapiens

<400> 467

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tcgggccaga attcggcacg aggcggcacg agggcgacgg cctcacgggg 50

ctttggaggt gaaagaggcc cagagtagag agagagagag accgacgtac 100

acgggatggc tacgggaacg cgctatgccg ggaaggtggt ggtcgtgacc 150

gggggcgggc gcggcatcgg agctgggatc gtgcgcgcct tcgtgaacag 200

cggggcccga gtggttatct gcgacaagga tgagtctggg ggccgggccc 250

tggagcagga gctccctgga gctgtcttta tcctctgtga tgtgactcag 300

gaagatgatg tgaagaccct ggtttctgag accatccgcc gatttggccg 350

cctggattgt gttgtcaaca acgctggcca ccacccaccc ccacagaggc 400
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ctgaggagac ctctgcccag ggattccgcc agctgctgga gctgaaccta 450

ctggggacgt acaccttgac caagctcgcc ctcccctacc tgcggaagag 500

tcaagggaat gtcatcaaca tctccagcct ggtgggggca atcggccagg 550

cccaggcagt tccctatgtg gccaccaagg gggcagtaac agccatgacc 600

aaagctttgg ccctggatga aagtccatat ggtgtccgag tcaactgtat 650

ctccccagga aacatctgga ccccgctgtg ggaggagctg gcagccttaa 700

tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750

ggccgcatgg gccagcccgc tgaggtcggg gctgcggcag tgttcctggc 800

ctccgaagcc aacttctgca cgggcattga actgctcgtg acgggggtg 850

cagagctggg gtacgggtgc aaggccagtc ggagcacccc cgtggacgcc 900

cccgatatcc cttcctgatt tctctcattt ctacttgggg ccccttcct 950

aggactctcc caccccaaac tccaacctgt atcagatgca gcccccaagc 1000

ccttagactc taagcccagt tagcaaggtg ccgggtcacc ctgcaggttc 1050

ccataaaaac gatttgcagc c 1071

<210> 468
<211> 270
<212> PRT
<213> Homo sapiens

<400> 468

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Met Ala Thr Gly Thr Arg Tyr Ala Gly Lys Val Val Val Val Thr
 1               5                  10                  15

Gly Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val
                20                  25                  30

Asn Ser Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly
                35                  40                  45

Gly Arg Ala Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu
                50                  55                  60

Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu
                65                  70                  75

Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala
                80                  85                  90

Gly His His Pro Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln
                95                 100                 105

Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr
               110                 115                 120
```

```
Leu Thr Lys Leu Ala Leu Pro Tyr Leu Arg Lys Ser Gln Gly Asn
                125                 130                 135

Val Ile Asn Ile Ser Ser Leu Val Gly Ala Ile Gly Gln Ala Gln
                140                 145                 150

Ala Val Pro Tyr Val Ala Thr Lys Gly Ala Val Thr Ala Met Thr
                155                 160                 165

Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly Val Arg Val Asn
                170                 175                 180

Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp Glu Glu Leu
                185                 190                 195

Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu Gly Met
                200                 205                 210

Leu Ala Gln Pro Leu Gly Arg Met Gly Gln Pro Ala Glu Val Gly
                215                 220                 225

Ala Ala Ala Val Phe Leu Ala Ser Glu Ala Asn Phe Cys Thr Gly
                230                 235                 240

Ile Glu Leu Leu Val Thr Gly Gly Ala Glu Leu Gly Tyr Gly Cys
                245                 250                 255

Lys Ala Ser Arg Ser Thr Pro Val Asp Ala Pro Asp Ile Pro Ser
                260                 265                 270
```

<210> 469
<211> 687
<212> DNA
<213> Homo sapiens

<400> 469

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aggcgggcag cagctgcagg ctgaccttgc agcttggcgg aatggactgg 50

cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100

ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150

ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200

aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250

ggcccagctg aggaacagct cagagctggc ccagagaaag tgtgaggtca 300

acttgcagct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350

agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400

gtgcctgtgt ctgggctgtg tgaacccctt caccatgcag gaggaccgca 450

gcatggtgag cgtgccggtg ttcagccagg ttcctgtgcg ccgccgcctc 500

tgcccgccac cgccccgcac agggccttgc cgccagcgcg cagtcatgga 550
```

```
gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600

gccaggccag cagcccgaga ccatcctcct tgcacctttg tgccaagaaa 650

ggcctatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470
<211> 180
<212> PRT
<213> Homo sapiens

<400> 470
Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile
1               5                   10                  15

Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys
                20                  25                  30

Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val
                35                  40                  45

Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu
                50                  55                  60

Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn
                65                  70                  75

Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu
                80                  85                  90

Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile
                95                  100                 105

Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg
                110                 115                 120

Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp
                125                 130                 135

Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg
                140                 145                 150

Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln
                155                 160                 165

Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
                170                 175                 180

<210> 471
<211> 2368
<212> DNA
<213> Homo sapiens

<400> 471
gcgccgccag gcgtaggcgg ggtggccctt gcgtctcccg cttccttgaa 50

aaacccggcg ggcgagcgag gctgcgggcc ggccgctgcc cttccccaca 100
```

ctccccgccg agaagcctcg ctcggcgccc aacatggcgg gtgggcgctg 150
cggcccgcag ctaacggcgc tcctggccgc ctggatcgcg gctgtggcgg 200
cgacggcagg ccccgaggag gccgcgctgc cgccggagca gagccgggtc 250
cagcccatga ccgcctccaa ctggacgctg gtgatggagg gcgagtggat 300
gctgaaattt tacgccccat ggtgtccatc ctgccagcag actgattcag 350
aatgggaggc ttttgcaaag aatggtgaaa tacttcagat cagtgtgggg 400
aaggtagatg tcattcaaga accaggtttg agtggccgct tctttgtcac 450
cactctccca gcattttttc atgcaaagga tgggatattc cgccgttatc 500
gtggcccagg aatcttcgaa gacctgcaga attatatctt agagaagaaa 550
tggcaatcag tcgagcctct gactggctgg aaatccccag cttctctaac 600
gatgtctgga atggctggtc tttttagcat ctctggcaag atatggcatc 650
ttcacaacta tttcacagtg actcttggaa ttcctgcttg gtgttcttat 700
gtgtttttcg tcatagccac cttggttttt ggccttttta tgggtctggt 750
cttggtggta atatcagaat gtttctatgt gccacttcca aggcatttat 800
ctgagcgttc tgagcagaat cggagatcag aggaggctca tagagctgaa 850
cagttgcagg atgcggagga ggaaaaagat gattcaaatg aagaagaaaa 900
caaagacagc cttgtagatg atgaagaaga gaaagaagat cttggcgatg 950
aggatgaagc agaggaagaa gaggaggagg acaacttggc tgctggtgtg 1000
gatgaggaga gaagtgaggc caatgatcag ggcccccag gagaggacgg 1050
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agcaaccctg cccagctgac acagaggtgg tggaagactc cttgaggcag 1150
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caagaataca caccaaaaca atatgtcagc ttccctttgg cctgcagttt 1250
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ctctctagtc atttggtctc atggcagtaa gcctcatgta tactaaggag 1350
agtcttccag gtgtgacaat caggatatag aaaaacaaac gtagtgttgg 1400
gatctgtttg gagactggga tgggaacaag ttcatttact taggggtcag 1450
agagtctcga ccagaggagg ccattcccag tcctaatcag caccttccag 1500
agacaaggct gcaggccctg tgaaatgaaa gccaagcagg agccttggct 1550

cctgagcatc cccaaagtgt aacgtagaag ccttgcatcc ttttcttgtg 1600

taaagtattt atttttgtca aattgcagga aacatcaggc accacagtgc 1650

atgaaaaatc tttcacagct agaaattgaa agggccttgg gtatagagag 1700

cagctcagaa gtcatcccag ccctctgaat ctcctgtgct atgttttatt 1750

tcttaccttt aatttttcca gcatttccac catgggcatt caggctctcc 1800

acactcttca ctattatctc ttggtcagag gactccaata acagccaggt 1850

ttacatgaac tgtgtttgtt cattctgacc taaggggttt agataatcag 1900

taaccataac ccctgaagct gtgactgcca aacatctcaa atgaaatgtt 1950

gtggccatca gagactcaaa aggaagtaag gattttacaa gacagattaa 2000

aaaaaaattg ttttgtccaa aatatagttg ttgttgattt ttttttaagt 2050

tttctaagca atatttttca agccagaagt cctctaagtc ttgccagtac 2100

aaggtagtct tgtgaagaaa agttgaatac tgttttgttt tcatctcaag 2150

gggttccctg ggtcttgaac tactttaata ataactaaaa aaccacttct 2200

gattttcctt cagtgatgtg cttttggtga aagaattaat gaactccagt 2250

acctgaaagt gaaagatttg attttgtttc catcttctgt aatcttccaa 2300

agaattatat ctttgtaaat ctctcaatac tcaatctact gtaagtaccc 2350

agggaggcta atttcttt 2368

<210> 472
<211> 349
<212> PRT
<213> Homo sapiens

<400> 472

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Met Ala Gly Gly Arg Cys Gly Pro Gln Leu Thr Ala Leu Leu Ala
 1               5                  10                  15

Ala Trp Ile Ala Ala Val Ala Ala Thr Ala Gly Pro Glu Glu Ala
                20                  25                  30

Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser
                35                  40                  45

Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr
                50                  55                  60

Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu
                65                  70                  75

Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys
                80                  85                  90
```

```
Val Asp Val Ile Gln Glu Pro Gly Leu Ser Gly Arg Phe Phe Val
                95                  100                 105

Thr Thr Leu Pro Ala Phe Phe His Ala Lys Asp Gly Ile Phe Arg
                110                 115                 120

Arg Tyr Arg Gly Pro Gly Ile Phe Glu Asp Leu Gln Asn Tyr Ile
                125                 130                 135

Leu Glu Lys Lys Trp Gln Ser Val Glu Pro Leu Thr Gly Trp Lys
                140                 145                 150

Ser Pro Ala Ser Leu Thr Met Ser Gly Met Ala Gly Leu Phe Ser
                155                 160                 165

Ile Ser Gly Lys Ile Trp His Leu His Asn Tyr Phe Thr Val Thr
                170                 175                 180

Leu Gly Ile Pro Ala Trp Cys Ser Tyr Val Phe Phe Val Ile Ala
                185                 190                 195

Thr Leu Val Phe Gly Leu Phe Met Gly Leu Val Leu Val Val Ile
                200                 205                 210

Ser Glu Cys Phe Tyr Val Pro Leu Pro Arg His Leu Ser Glu Arg
                215                 220                 225

Ser Glu Gln Asn Arg Arg Ser Glu Glu Ala His Arg Ala Glu Gln
                230                 235                 240

Leu Gln Asp Ala Glu Glu Glu Lys Asp Asp Ser Asn Glu Glu Glu
                245                 250                 255

Asn Lys Asp Ser Leu Val Asp Asp Glu Glu Glu Lys Glu Asp Leu
                260                 265                 270

Gly Asp Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Asp Asn Leu
                275                 280                 285

Ala Ala Gly Val Asp Glu Glu Arg Ser Glu Ala Asn Asp Gln Gly
                290                 295                 300

Pro Pro Gly Glu Asp Gly Val Thr Arg Glu Glu Val Glu Pro Glu
                305                 310                 315

Glu Ala Glu Glu Gly Ile Ser Glu Gln Pro Cys Pro Ala Asp Thr
                320                 325                 330

Glu Val Val Glu Asp Ser Leu Arg Gln Arg Lys Ser Gln His Ala
                335                 340                 345

Asp Lys Gly Leu


<210> 473
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic oligonucleotide probe

<400> 473
gtccagccca tgaccgcctc caac 24

<210> 474
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 474
ctctcctcat ccacaccagc agcc 24

<210> 475
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 475
gtggatgctg aaattttacg ccccatggtg tccatcctgc cagc 44

<210> 476
<211> 2478
<212> DNA
<213> Homo sapiens

<400> 476
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gcccacatga tttgactcag agattctctt ttgtccacag acagtcatct 100

caggggcaga aagaaaagag ctcccaaatg ctatatctat tcaggggctc 150

tcaagaacaa tggaatatca tcctgattta gaaaatttgg atgaagatgg 200

atatactcaa ttacacttcg actctcaaag caataccagg atagctgttg 250

tttcagagaa aggatcgtgt gctgcatctc ctccttggcg cctcattgct 300

gtaattttgg gaatcctatg cttggtaata ctggtgatag ctgtggtcct 350

gggtaccatg gggggttcttt ccagcccttg tcctcctaat tggattatat 400

atgagaagag ctgttatcta ttcagcatgt cactaaattc ctgggatgga 450

agtaaaagac aatgctggca actgggctct aatctcctaa agatagacag 500

ctcaaatgaa ttgggattta tagtaaaaca agtgtcttcc caacctgata 550

attcattttg gataggcctt tctcggcccc agactgaggt accatggctc 600 tgggaggatg gatcaacatt ctcttctaac ttatttcaga tcagaaccac 650

agctacccaa gaaaacccat ctccaaattg tgtatggatt cacgtgtcag 700

tcatttatga ccaactgtgt agtgtgccct catatagtat ttgtgagaag 750

aagttttcaa tgtaagagga agggtggaga aggagagaga aatatgtgag 800

gtagtaagga ggacagaaaa cagaacagaa aagagtaaca gctgaggtca 850

agataaatgc agaaaatgtt tagagagctt ggccaactgt aatcttaacc 900

aagaaattga agggagaggc tgtgatttct gtatttgtcg acctacaggt 950

aggctagtat tatttttcta gttagtagat ccctagacat ggaatcaggg 1000

cagccaagct tgagttttta tttttattt atttattttt ttgagatagg 1050

gtctcacttt gttacccagg ctggagtgca gtggcacaat ctcgactcac 1100

tgcagctatc tctcgcctca gcccctcaag tagctgggac tacaggtgca 1150

tgccaccatg ccaggctaat ttttggtgtt ttttgtagag actgggtttt 1200

gccatgttga ccaagctggt ctctaactcc tgggcttaag tgatctgccc 1250

gccttggcct cccaaagtgc tgggattaca gatgtgagcc accacacctg 1300

gccccaagct tgaattttca ttctgccatt gacttggcat ttaccttggg 1350

taagccataa gcgaatctta atttctggct ctatcagagt tgtttcatgc 1400

tcaacaatgc cattgaagtg cacggtgtgt tgccacgatt tgaccctcaa 1450

cttctagcag tatatcagtt atgaactgag ggtgaaatat atttctgaat 1500

agctaaatga agaaatggga aaaaatcttc accacagtca gagcaatttt 1550

attattttca tcagtatgat cataattatg attatcatct tagtaaaaag 1600

caggaactcc tactttttct ttatcaatta aatagctcag agagtacatc 1650

tgccatatct ctaatagaat cttttttttt tttttttttt tttgagacag 1700

agtttcgctc ttgttgccca ggctggagtg caacggcacg atctcggctc 1750

accgcaacct ccgcccctg ggttcaagca attctcctgc ctcagcctcc 1800

caagtagctg ggattacagt caggcaccac cacacccggc taattttgta 1850

ttttttagt agagacaggg tttctccatg tcggtcaggg tagtcccgaa 1900

ctcctgacct caagtgatct gcctgcctcg gcctcccaag tgctgggatt 1950

acaggcgtga gccactgcac ccagcctaga atcttgtata atatgtaatt 2000

gtagggaaac tgctctcata ggaaagtttt ctgcttttta aatacaaaaa 2050

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tacataaaaa tacataaaat ctgatgatga atataaaaaa gtaaccaacc 2100

tcattggaac aagtattaac attttggaat atgttttatt agttttgtga 2150

tgtactgttt tacaattttt accatttttt tcagtaatta ctgtaaaatg 2200

gtattattgg aatgaaacta tatttcctca tgtgctgatt tgtcttattt 2250

ttttcatact ttcccactgg tgctattttt atttccaatg gatatttctg 2300

tattactagg gaggcattta cagtcctcta atgttgatta atatgtgaaa 2350

agaaattgta ccaattttac taaattatgc agtttaaaat ggatgatttt 2400

atgttatgtg gatttcattt caataaaaaa aaactcttat caaaaaaaaa 2450

aaaaaaaaaa aaaaaaaaaa aaaaaaaa 2478

<210> 477
<211> 201
<212> PRT
<213> Homo sapiens

<400> 477
Met Glu Tyr His Pro Asp Leu Glu Asn Leu Asp Glu Asp Gly Tyr
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Thr Gln Leu His Phe Asp Ser Gln Ser Asn Thr Arg Ile Ala Val
                20                  25                  30

Val Ser Glu Lys Gly Ser Cys Ala Ala Ser Pro Pro Trp Arg Leu
                35                  40                  45

Ile Ala Val Ile Leu Gly Ile Leu Cys Leu Val Ile Leu Val Ile
                50                  55                  60

Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro
                65                  70                  75

Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met
                80                  85                  90

Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu
                95                 100                 105

Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe
               110                 115                 120

Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile
               125                 130                 135

Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp
               140                 145                 150

Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala
               155                 160                 165

Thr Gln Glu Asn Pro Ser Pro Asn Cys Val Trp Ile His Val Ser
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170 175 180

Val Ile Tyr Asp Gln Leu Cys Ser Val Pro Ser Tyr Ser Ile Cys
185 190 195

Glu Lys Lys Phe Ser Met
200

<210> 478
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 478
gtccacagac agtcatctca ggagcag 27

<210> 479
<211> 20
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 479
acaagtgtct tcccaacctg 20

<210> 480
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<212> DNA
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<223> Synthetic oligonucleotide probe

<400> 480
atcctcccag agccatggta cctc 24

<210> 481
<211> 51
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 481
ccaaggatag ctgttgtttc agagaaagga tcgtgtgctg catctcctcc 50

t 51

<210> 482
<211> 3819
<212> DNA
<213> Homo sapiens

<400> 482
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tcttggctca tcgtaacctc cacctcccgg gttcaagtga ttctcatgcc 150

tcagcctccc gagtagctgg gattacaggt ggtgacttcc aagagtgact 200

ccgtcggagg aaaatgactc cccagtcgct gctgcagacg acactgttcc 250

tgctgagtct gctcttcctg gtccaaggtg cccacggcag gggccacagg 300

gaagactttc gcttctgcag ccagcggaac cagacacaca ggagcagcct 350

ccactacaaa cccacaccag acctgcgcat ctccatcgag aactccgaag 400

aggccctcac agtccatgcc cctttccctg cagcccaccc tgcttcccga 450

tccttccctg accccagggg cctctaccac ttctgcctct actggaaccg 500

acatgctggg agattacatc ttctctatgg caagcgtgac ttcttgctga 550

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gaggaccgga tcaacgccac ggtgtggaag ctccagccca cagccggcct 950

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tggggattgt ggtacagaac accaaagtag ccaacctcac ggagcccgtg 1200

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tgtgttctgg gttgaagacc ccacattgag cagcccgggg cattggagca 1300

gtgctgggtg tgagaccgtc aggagagaaa cccaaacatc ctgcttctgc 1350

aaccacttga cctactttgc agtgctgatg gtctcctcgg tggaggtgga 1400

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tcccaccact ccaaggactg agactgacct cctctggtga cactggccta 3300

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ggtagattgc tggcctgttg taggtggtag ggacacagat gaccgacctg 3450

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3800

aaaaaaaaaa aaaaaaaaa 3819
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<210> 483
<211> 693
<212> PRT
<213> Homo sapiens

<400> 483
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   1               5                  10                  15

 Leu Leu Phe Leu Val Gln Gly Ala His Gly Arg Gly His Arg Glu
                  20                  25                  30

 Asp Phe Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser
                  35                  40                  45

 Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn
                  50                  55                  60

 Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His
                  65                  70                  75
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Pro Ala Ser Arg Ser Phe Pro Asp Pro Arg Gly Leu Tyr His Phe
                80   85   90

Cys Leu Tyr Trp Asn Arg His Ala Gly Arg Leu His Leu Leu Tyr
                95   100   105

Gly Lys Arg Asp Phe Leu Leu Ser Asp Lys Ala Ser Ser Leu Leu
                110   115   120

Cys Phe Gln His Gln Glu Glu Ser Leu Ala Gln Gly Pro Pro Leu
                125   130   135

Leu Ala Thr Ser Val Thr Ser Trp Trp Ser Pro Gln Asn Ile Ser
                140   145   150

Leu Pro Ser Ala Ala Ser Phe Thr Phe Ser Phe His Ser Pro Pro
                155   160   165

His Thr Ala Ala His Asn Ala Ser Val Asp Met Cys Glu Leu Lys
                170   175   180

Arg Asp Leu Gln Leu Leu Ser Gln Phe Leu Lys His Pro Gln Lys
                185   190   195

Ala Ser Arg Arg Pro Ser Ala Ala Pro Ala Ser Gln Gln Leu Gln
                200   205   210

Ser Leu Glu Ser Lys Leu Thr Ser Val Arg Phe Met Gly Asp Met
                215   220   225

Val Ser Phe Glu Glu Asp Arg Ile Asn Ala Thr Val Trp Lys Leu
                230   235   240

Gln Pro Thr Ala Gly Leu Gln Asp Leu His Ile His Ser Arg Gln
                245   250   255

Glu Glu Glu Gln Ser Glu Ile Met Glu Tyr Ser Val Leu Leu Pro
                260   265   270

Arg Thr Leu Phe Gln Arg Thr Lys Gly Arg Ser Gly Glu Ala Glu
                275   280   285

Lys Arg Leu Leu Leu Val Asp Phe Ser Ser Gln Ala Leu Phe Gln
                290   295   300

Asp Lys Asn Ser Ser Gln Val Leu Gly Glu Lys Val Leu Gly Ile
                305   310   315

Val Val Gln Asn Thr Lys Val Ala Asn Leu Thr Glu Pro Val Val
                320   325   330

Leu Thr Phe Gln His Gln Leu Gln Pro Lys Asn Val Thr Leu Gln
                335   340   345

Cys Val Phe Trp Val Glu Asp Pro Thr Leu Ser Ser Pro Gly His
                350   355   360

Trp Ser Ser Ala Gly Cys Glu Thr Val Arg Arg Glu Thr Gln Thr

365 370 375

Ser Cys Phe Cys Asn His Leu Thr Tyr Phe Ala Val Leu Met Val
380 385 390

Ser Ser Val Glu Val Asp Ala Val His Lys His Tyr Leu Ser Leu
395 400 405

Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu Ala Cys Leu Val
410 415 420

Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu Pro Cys Arg
425 430 435

Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn Leu Leu
440 445 450

Leu Ala Val Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu Pro
455 460 465

Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile
470 475 480

Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu
485 490 495

Glu Gly Tyr Asn Leu Tyr Arg Leu Val Val Glu Val Phe Gly Thr
500 505 510

Tyr Val Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly
515 520 525

Phe Pro Ile Phe Leu Val Thr Leu Val Ala Leu Val Asp Val Asp
530 535 540

Asn Tyr Gly Pro Ile Ile Leu Ala Val His Arg Thr Pro Glu Gly
545 550 555

Val Ile Tyr Pro Ser Met Cys Trp Ile Arg Asp Ser Leu Val Ser
560 565 570

Tyr Ile Thr Asn Leu Gly Leu Phe Ser Leu Val Phe Leu Phe Asn
575 580 585

Met Ala Met Leu Ala Thr Met Val Val Gln Ile Leu Arg Leu Arg
590 595 600

Pro His Thr Gln Lys Trp Ser His Val Leu Thr Leu Leu Gly Leu
605 610 615

Ser Leu Val Leu Gly Leu Pro Trp Ala Leu Ile Phe Phe Ser Phe
620 625 630

Ala Ser Gly Thr Phe Gln Leu Val Val Leu Tyr Leu Phe Ser Ile
635 640 645

Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile Trp Tyr Trp Ser
650 655 660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn
                665   670   675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser
                680   685   690

Ser Arg Ile

<210> 484
<211> 516
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 68, 70, 84, 147
<223> unknown base

<400> 484
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ctgccttgca gaggaaancn tcgggactac accntcaagt gcacatgaac 100

ctgctgctgg ccgtcttcct gctggacacg agcttcctgc tcagcgnagc 150

cggtggccct gacaggctct gaaggctggc tgccgagcca gtgccatctt 200

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caacctctac cgactcgtgg tggaggtctt tggcacctat gtccctggct 300

acctactcaa gctgagcgcc atgggctggg gcttccccat ctttctggtg 350

acgctggtgg ccctggtgga tgtggacaac tatggcccca tcatcttggc 400

tgtgcatagg actccagagg gcgtcatcta cccttccatg tgctggatcc 450

gggactccct ggtcagctac atcaccaacc tgggcctctt cagcctggtg 500

tttctgttca acatgg 516

<210> 485
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 485
ggcattggag cagtgctggg tg 22

<210> 486
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 486
tggaggccta gatgcggctg gacg 24

<210> 487
<211> 2849
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2715
<223> unknown base

<400> 487
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ggttcaggtc caggttttgc tttgatcctt ttcaaaaact ggagacacag 100

aagagggctc taggaaaaag ttttggatgg gattatgtgg aaactaccct 150

gcgattctct gctgccagag caggctcggc gcttccaccc cagtgcagcc 200

ttcccctggc ggtggtgaaa gagactcggg agtcgctgct tccaaagtgc 250

ccgccgtgag tgagctctca ccccagtcag ccaaatgagc ctcttcgggc 300

ttctcctgct gacatctgcc ctggccggcc agagacaggg gactcaggcg 350

gaatccaacc tgagtagtaa attccagttt tccagcaaca aggaacagaa 400

cggagtacaa gatcctcagc atgagagaat tattactgtg tctactaatg 450

gaagtattca cagcccaagg tttcctcata cttatccaag aaatacggtc 500

ttggtatgga gattagtagc agtagaggaa aatgtatgga tacaacttac 550

gtttgatgaa agatttgggc ttgaagaccc agaagatgac atatgcaagt 600

atgattttgt agaagttgag gaacccagtg atggaactat attagggcgc 650

tggtgtggtt ctggtactgt accaggaaaa cagatttcta aaggaaatca 700

aattaggata agatttgtat ctgatgaata ttttccttct gaaccagggt 750

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tcactcaccg acgtggccct ggagcaccat gaggagtgtg actgtgtgtg 1300

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gtggaaagaa aattaaatgt tgtattaaat agatcaccag ctagtttcag 1600

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atctgagcct agctcagaaa aacataaagc accttgaaaa agacttggca 2500

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aaaaaaaaaa aaaaaaaaaa aggtttaggg ataacagggt aatgcggcc 2849

<210> 488
<211> 345
<212> PRT
<213> Homo sapiens

<400> 488
Met Ser Leu Phe Gly Leu Leu Leu Leu Thr Ser Ala Leu Ala Gly
  1               5                  10                  15

Gln Arg Gln Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys Phe
                 20                  25                  30

Gln Phe Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln
                 35                  40                  45

His Glu Arg Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser
                 50                  55                  60

Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp
                 65                  70                  75

Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln Leu Thr Phe
                 80                  85                  90

Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys Lys
                 95                 100                 105

Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile Leu
                110                 115                 120

Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser
                125                 130                 135

Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe
                140                 145                 150

Pro Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro
                155                 160                 165

Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala
                170                 175                 180

Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr
                185                 190                 195
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Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu
                200                 205                 210

Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys
                215                 220                 225

Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu
                230                 235                 240

Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe
                245                 250                 255

Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe
                260                 265                 270

Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala
                275                 280                 285

Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys
                290                 295                 300

Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr
                305                 310                 315

Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu
                320                 325                 330

His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly
                335                 340                 345
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<210> 489
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 489
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<210> 490
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 490
gaactaaaga gaaccgatac cattttctgg ccaggttgtc 40

<210> 491
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491
caccacagcg tttaaccagg 20

<210> 492
<211> 20
<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<213> Homo sapiens

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ggacactgaa gagacaaatt cttatccttt ttaacataat cctaatttcc 150

aaactccttg ggctagatg gtttcctaaa actctgccct gtgatgtcac 200

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tgacagaaat tcctggaggt attcccacga acaccacgaa cctcaccctc 300

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ggctctgtgg gagttctgtc cttgagtggc caacaaaccc gcaagctcac 3150

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 Phe Asn Ile Ile Leu Ile Ser Lys Leu Leu Gly Ala Arg Trp Phe
                  20                  25                  30

 Pro Lys Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn
                  35                  40                  45

 His Val Ile Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro
                  50                  55                  60

 Gly Gly Ile Pro Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn
                  65                  70                  75

 His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His
                  80                  85                  90

 Leu Val Glu Ile Asp Phe Arg Cys Asn Cys Val Pro Ile Pro Leu
                  95                 100                 105

 Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu Gln Ile Lys Pro
                 110                 115                 120

 Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu Tyr Leu Asp
                 125                 130                 135

 Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro Ser Leu
                 140                 145                 150

 Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg Lys
                 155                 160                 165

 Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly
                 170                 175                 180

 Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile
                 185                 190                 195

 Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser
                 200                 205                 210

 Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser
                 215                 220                 225

 Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile
                 230                 235                 240

 Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp
                 245                 250                 255
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Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys
                260                 265                 270

Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala
                275                 280                 285

Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn
                290                 295                 300

Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys
                305                 310                 315

Leu Gln Glu Leu Asp Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile
                320                 325                 330

Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu
                335                 340                 345

Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr Arg Ala Ser Met
                350                 355                 360

Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu Lys Ile Leu
                365                 370                 375

Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu
                380                 385                 390

Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly
                395                 400                 405

Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe
                410                 415                 420

Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro
                425                 430                 435

Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr
                440                 445                 450

Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr
                455                 460                 465

Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys
                470                 475                 480

Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly
                485                 490                 495

Gln Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser
                500                 505                 510

Ser Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser
                515                 520                 525

Gly Asn Leu Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro
                530                 535                 540

Leu Ala Glu Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp
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545 550 555

Leu Leu His Ser Thr Ala Phe Glu Glu Leu His Lys Leu Glu Val
560 565 570

Leu Asp Ile Ser Ser Asn Ser His Tyr Phe Gln Ser Glu Gly Ile
575 580 585

Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys Val Leu Gln Lys
590 595 600

Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr Ser Arg Thr
605 610 615

Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly Asn His
620 625 630

Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln Leu
635 640 645

Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn
650 655 660

Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro
665 670 675

Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe
680 685 690

Ser Trp Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp
695 700 705

Leu Ser His Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn
710 715 720

Cys Ser Arg Ser Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile
725 730 735

Arg Ser Leu Thr Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg
740 745 750

Tyr Leu Asp Leu Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr
755 760 765

Ser Phe Pro Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu
770 775 780

His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val
785 790 795

Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr
800 805 810

Asp Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val
815 820 825

Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp Leu Thr Asn Leu
830 835 840

Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val
845 850 855

Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp Tyr Ile
860 865 870

Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile
875 880 885

Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys
890 895 900

Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys
905 910 915

Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu
920 925 930

Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln
935 940 945

Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys
950 955 960

Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His
965 970 975

Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe
980 985 990

Leu Glu Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys
995 1000 1005

Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln
1010 1015 1020

Ala His Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Ala Thr
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Asp Asn His Val Ala Tyr Ser Gln Val Phe Lys Glu Thr Val
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<213> Homo sapiens

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cctgctaata tctggttcct gtgagttatg cgccgaagaa aatttttcta 150

gaagctatcc ttgtgatgag aaaaagcaaa atgactcagt tattgcagag 200

tgcagcaatc gtcgactaca ggaagttccc caaacggtgg gcaaatatgt 250 gacagaacta gacctgtctg ataatttcat cacacacata acgaatgaat 300

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attttaacaa agtttgcgag aaaactaaca tagaagatgg agtatttgaa 650

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cgtgccaccc aaactgccaa gctccctacg caaacttttt ctgagcaaca 750

cccagatcaa atacattagt gaagaagatt tcaagggatt gataaattta 800

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<211> 1041
<212> PRT
<213> Homo sapiens

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                20                  25                  30

Ser Arg Ser Tyr Pro Cys Asp Glu Lys Lys Gln Asn Asp Ser Val
                35                  40                  45

Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr
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                    50                  55                  60

Val Gly Lys Tyr Val Thr Glu Leu Asp Leu Ser Asp Asn Phe Ile
                65                  70                  75

Thr His Ile Thr Asn Glu Ser Phe Gln Gly Leu Gln Asn Leu Thr
                80                  85                  90

Lys Ile Asn Leu Asn His Asn Pro Asn Val Gln His Gln Asn Gly
                95                  100                 105

Asn Pro Gly Ile Gln Ser Asn Gly Leu Asn Ile Thr Asp Gly Ala
                110                 115                 120

Phe Leu Asn Leu Lys Asn Leu Arg Glu Leu Leu Leu Glu Asp Asn
                125                 130                 135

Gln Leu Pro Gln Ile Pro Ser Gly Leu Pro Glu Ser Leu Thr Glu
                140                 145                 150

Leu Ser Leu Ile Gln Asn Asn Ile Tyr Asn Ile Thr Lys Glu Gly
                155                 160                 165

Ile Ser Arg Leu Ile Asn Leu Lys Asn Leu Tyr Leu Ala Trp Asn
                170                 175                 180

Cys Tyr Phe Asn Lys Val Cys Glu Lys Thr Asn Ile Glu Asp Gly
                185                 190                 195

Val Phe Glu Thr Leu Thr Asn Leu Glu Leu Leu Ser Leu Ser Phe
                200                 205                 210

Asn Ser Leu Ser His Val Pro Pro Lys Leu Pro Ser Ser Leu Arg
                215                 220                 225

Lys Leu Phe Leu Ser Asn Thr Gln Ile Lys Tyr Ile Ser Glu Glu
                230                 235                 240

Asp Phe Lys Gly Leu Ile Asn Leu Thr Leu Leu Asp Leu Ser Gly
                245                 250                 255

Asn Cys Pro Arg Cys Phe Asn Ala Pro Phe Pro Cys Val Pro Cys
                260                 265                 270

Asp Gly Gly Ala Ser Ile Asn Ile Asp Arg Phe Ala Phe Gln Asn
                275                 280                 285

Leu Thr Gln Leu Arg Tyr Leu Asn Leu Ser Ser Thr Ser Leu Arg
                290                 295                 300

Lys Ile Asn Ala Ala Trp Phe Lys Asn Met Pro His Leu Lys Val
                305                 310                 315

Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly Glu Ile Val Ser Gly
                320                 325                 330

Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile Leu Asp Leu Ser
                335                 340                 345
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Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile Asn Ile Ser
                350                 355                 360

Arg Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His Leu Arg
                365                 370                 375

Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro Leu
                380                 385                 390

Met Gln Leu Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe
                395                 400                 405

Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu
                410                 415                 420

Glu Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro Leu Val Lys
                425                 430                 435

Asp Thr Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln Arg His
                440                 445                 450

Ile Arg Lys Arg Arg Ser Thr Asp Phe Glu Phe Asp Pro His Ser
                455                 460                 465

Asn Phe Tyr His Phe Thr Arg Pro Leu Ile Lys Pro Gln Cys Ala
                470                 475                 480

Ala Tyr Gly Lys Ala Leu Asp Leu Ser Leu Asn Ser Ile Phe Phe
                485                 490                 495

Ile Gly Pro Asn Gln Phe Glu Asn Leu Pro Asp Ile Ala Cys Leu
                500                 505                 510

Asn Leu Ser Ala Asn Ser Asn Ala Gln Val Leu Ser Gly Thr Glu
                515                 520                 525

Phe Ser Ala Ile Pro His Val Lys Tyr Leu Asp Leu Thr Asn Asn
                530                 535                 540

Arg Leu Asp Phe Asp Asn Ala Ser Ala Leu Thr Glu Leu Ser Asp
                545                 550                 555

Leu Glu Val Leu Asp Leu Ser Tyr Asn Ser His Tyr Phe Arg Ile
                560                 565                 570

Ala Gly Val Thr His His Leu Glu Phe Ile Gln Asn Phe Thr Asn
                575                 580                 585

Leu Lys Val Leu Asn Leu Ser His Asn Asn Ile Tyr Thr Leu Thr
                590                 595                 600

Asp Lys Tyr Asn Leu Glu Ser Lys Ser Leu Val Glu Leu Val Phe
                605                 610                 615

Ser Gly Asn Arg Leu Asp Ile Leu Trp Asn Asp Asp Asp Asn Arg
                620                 625                 630

Tyr Ile Ser Ile Phe Lys Gly Leu Lys Asn Leu Thr Arg Leu Asp
```

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                635                 640                 645

Leu Ser Leu Asn Arg Leu Lys His Ile Pro Asn Glu Ala Phe Leu
                650                 655                 660

Asn Leu Pro Ala Ser Leu Thr Glu Leu His Ile Asn Asp Asn Met
                665                 670                 675

Leu Lys Phe Phe Asn Trp Thr Leu Leu Gln Gln Phe Pro Arg Leu
                680                 685                 690

Glu Leu Leu Asp Leu Arg Gly Asn Lys Leu Leu Phe Leu Thr Asp
                695                 700                 705

Ser Leu Ser Asp Phe Thr Ser Ser Leu Arg Thr Leu Leu Leu Ser
                710                 715                 720

His Asn Arg Ile Ser His Leu Pro Ser Gly Phe Leu Ser Glu Val
                725                 730                 735

Ser Ser Leu Lys His Leu Asp Leu Ser Ser Asn Leu Leu Lys Thr
                740                 745                 750

Ile Asn Lys Ser Ala Leu Glu Thr Lys Thr Thr Thr Lys Leu Ser
                755                 760                 765

Met Leu Glu Leu His Gly Asn Pro Phe Glu Cys Thr Cys Asp Ile
                770                 775                 780

Gly Asp Phe Arg Arg Trp Met Asp Glu His Leu Asn Val Lys Ile
                785                 790                 795

Pro Arg Leu Val Asp Val Ile Cys Ala Ser Pro Gly Asp Gln Arg
                800                 805                 810

Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp
                815                 820                 825

Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr
                830                 835                 840

Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp
                845                 850                 855

Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr
                860                 865                 870

Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser
                875                 880                 885

Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu
                890                 895                 900

Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu
                905                 910                 915

Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp
                920                 925                 930
```

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Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val
                935                 940                 945

Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe
                950                 955                 960

Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile
                965                 970                 975

Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu
                980                 985                 990

Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro
                995                 1000                1005

Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn
                1010                1015                1020

Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val
                1025                1030                1035

Asp Ser Ile Lys Gln Tyr
                1040
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<210> 499
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 499
taaagaccca gctgtgaccg 20

<210> 500
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 500
atccatgagc ctctgatggg 20

<210> 501
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 501
atttatgtct cgaggaaagg gactggttac cagggcagcc agttc 45

<210> 502

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 502
gccgagacaa aaacgttctc c 21

<210> 503
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 503
catccatgtt ctcatccatt agcc 24

<210> 504
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 504
tcgacaacct catgcagagc atcaaccaaa gcaagaaaac agtatt 46

<210> 505
<211> 1738
<212> DNA
<213> Homo sapiens

<400> 505
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ctagagatcc ctcgacctcg acccacgcgt ccgccaagct ggccctgcac 100

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gtgcctccag gcggccagtg ggcctgaggc cccagcaagg gctagggtcc 200

atctccagtc ccaggacaca gcagcggcca ccatggccac gcctgggctc 250

cagcagcatc agcagccccc aggaccgggg aggcacaggt ggcccccacc 300

acccggagga gcagctcctg cccctgtccg gggatgact gattctcctc 350

cgccaggcca cccagaggag aaggccaccc cgcctggagg cacaggccat 400

gaggggctct caggaggtgc tgctgatgtg gcttctggtg ttggcagtgg 450

gcggcacaga gcacgcctac cggcccggcc gtagggtgtg tgctgtccgg 500 gctcacgggg accctgtctc cgagtcgttc gtgcagcgtg tgtaccagcc 550

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tggccccact gcacagcctg gcctcgcagg cactggagca tgggctcccg 1100

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agctccctgc tggagcctgg gacccatggc acaggccagg cagcccggag 1550

gctgggtggg gcctcagtgg gggctgctgc ctgaccccca gcacaataaa 1600

aatgaaacgt gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650

aaagggcggc cgcgactcta gagtcgacct gcagaagctt ggccgccatg 1700

gcccaacttg tttattgcag cttataatgg ttacaaat 1738

<210> 506
<211> 273
<212> PRT
<213> Homo sapiens

<400> 506
Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu
1   5   10   15

```
Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val
                20                  25                  30

Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
                35                  40                  45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
                50                  55                  60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
                65                  70                  75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
                80                  85                  90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
                95                  100                 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro
                110                 115                 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
                125                 130                 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln
                140                 145                 150

Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu
                155                 160                 165

Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly
                170                 175                 180

Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala
                185                 190                 195

Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu
                200                 205                 210

Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala
                215                 220                 225

Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu
                230                 235                 240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu
                245                 250                 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys
                260                 265                 270

Lys Asp Ser
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<210> 507
<211> 1700
<212> DNA
<213> Homo sapiens

<400> 507
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ccaccatggc cacgcctggg ctccagcagc atcagagcag cccctgtggt 150

tggcagcaaa gttcagcttg gctgggcccg ctgtgagggg cttcgcgcta 200

cgccctgcgg tgtcccgagg gctgaggtct cctcatcttc tccctagcag 250

tggatgagca acccaacggg ggcccgggga ggggaactgg ccccgaggga 300

gaggaacccc aaagccacat ctgtagccag gatgagcagt gtgaatccag 350

gcagccccca ggaccgggga ggcacaggtg gcccccacca cccggaggag 400

cagctcctgc ccctgtccgg gggatgactg attctcctcc gccaggccac 450

ccagaggaga aggccacccc gcctggaggc acaggccatg aggggctctc 500

aggaggtgct gctgatgtgg cttctggtgt tggcagtggg cggcacagag 550

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gcctaccgcc gcagccctgg gctggcccct gccaggcctc gctacgcgtg 750

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gacggtacac tctgtgtgcc caagggaggg ccccccaggg tggcccccaa 1050

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gactcgtgac tgcccagcgc tccaggctgg actgagcccc tcacgccgcc 1350

ctgcagcccc catgcccctg cccaacatgc tgggggtcca gaagccacct 1400

cggggtgact gagcggaagg ccaggcaggg ccttcctcct cttcctcctc 1450

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cccttcctcg ggaggctccc cagaccctgg catgggatgg gctgggatct 1500

tctctgtgaa tccacccctg gctacccccа ccctggctac cccaacggca 1550

tcccaaggcc aggtggaccc tcagctgagg gaaggtacga gctccctgct 1600

ggagcctggg acccatggca caggccaggc agcccggagg ctgggtgggg 1650

cctcagtggg ggctgctgcc tgacccccag cacaataaaa atgaaacgtg 1700

<210> 508
<211> 273
<212> PRT
<213> Homo sapiens

<400> 508
Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu
1               5                   10                  15

Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val
                20                  25                  30

Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
                35                  40                  45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
                50                  55                  60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
                65                  70                  75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
                80                  85                  90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
                95                  100                 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro
                110                 115                 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
                125                 130                 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln
                140                 145                 150

Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu
                155                 160                 165

Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly
                170                 175                 180

Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala
                185                 190                 195

Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu
                200                 205                 210
```

```
Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala
                215                 220                 225

Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu
                230                 235                 240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu
                245                 250                 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys
                260                 265                 270

Lys Asp Ser
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<210> 509
<211> 1538
<212> DNA
<213> Homo sapiens

<400> 509
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acaggccagg caggtgggcc tcaggaggtg cctccaggcg gccagtgggc 100

ctgaggcccc agcaagggct agggtccatc tccagtccca ggacacagca 150

gcggccacca tggccacgcc tgggctccag cagcatcagc agcccccagg 200

accggggagg cacaggtggc ccccaccacc cggaggagca gctcctgccc 250

ctgtccgggg gatgactgat tctcctccgc caggccaccc agaggagaag 300

gccaccccgc ctggaggcac aggccatgag ggctctcag gaggtgctgc 350

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gaagaggacc agcgggcttc ctggggcctg tggagcagca atatgccagc 650

cgccatgccg gaacggaggg agctgtgtcc agcctggccg ctgccgctgc 700

cctgcaggat ggcggggtga cacttgccag tcagatgtgg atgaatgcag 750

tgctaggagg ggcggctgtc cccagcgctg cgtcaacacc gccggcagtt 800

actggtgcca gtgttgggag gggcacagcc tgtctgcaga cggtacactc 850

tgtgtgccca agggagggcc ccccagggtg gcccccaacc cgacaggagt 900

ggacagtgca atgaaggaag aagtgcagag gctgcagtcc agggtggacc 950
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tgctggagga gaagctgcag ctggtgctgg ccccactgca cagcctggcc 1000

tcgcaggcac tggagcatgg gctcccggac cccggcagcc tcctggtgca 1050

ctccttccag cagctcggcc gcatcgactc cctgagcgag cagatttcct 1100

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cacccctggc tacccccacc ctggctaccc caacggcatc ccaaggccag 1400

gtgggccctc agctgaggga aggtacgagc tccctgctgg agcctgggac 1450

ccatggcaca ggccaggcag cccggaggct gggtggggcc tcagtggggg 1500

ctgctgcctg acccccagca caataaaaat gaaacgtg 1538

<210> 510
<211> 273
<212> PRT
<213> Homo sapiens

<400> 510

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Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu
 1               5                  10                  15

Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val
                20                  25                  30

Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
                35                  40                  45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
                50                  55                  60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
                65                  70                  75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
                80                  85                  90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
                95                 100                 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro
               110                 115                 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
               125                 130                 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln
```

```
                140                 145                 150

Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu
                155                 160                 165

Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly
                170                 175                 180

Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala
                185                 190                 195

Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu
                200                 205                 210

Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala
                215                 220                 225

Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu
                230                 235                 240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu
                245                 250                 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys
                260                 265                 270

Lys Asp Ser
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<210> 511
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 511
tggagcagca atatgccagc c 21

<210> 512
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 512
ttttccactc ctgtcgggtt gg 22

<210> 513
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 513
ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514
<211> 2690
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2039-2065
<223> unknown base

<400> 514
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agttgggtct ccgtgtttca ggccggctcc cccttcctgg tctcccttct 200

cccgctgggc cggtttatcg ggaggagatt gtcttccagg gctagcaatt 250

ggacttttga tgatgtttga cccagcggca ggaatagcag gcaacgtgat 300

ttcaaagctg ggctcagcct ctgtttcttc tctcgtgtaa tcgcaaaacc 350

cattttggag caggaattcc aatcatgtct gtgatggtgg tgagaaagaa 400

ggtgacacgg aaatgggaga aactcccagg caggaacacc ttttgctgtg 450

atggccgcgt catgatggcc cggcaaaagg gcattttcta cctgaccctt 500

ttcctcatcc tggggacatg tacactcttc ttcgcctttg agtgccgcta 550

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agaagctacc aatggtgcgg tgccccaggg ccagcgacca ccgcctcgta 750

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acatgcaaga tcttccggcc tccccgggcc tcccattgca gcatctgtga 850

caactgtgtg gagcgcttcg accatcactg cccctgggtg gggaattgtg 900

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catcaaagga tcatggacag ggaagaatcg cgtccagaat ccctacagcc 1200

atggcaatat tgtgaagaac tgctgtgaag tgctgtgtgg ccccttgccc 1250

cccagtgtgc tggatcgaag ggtattttg ccactggagg aaagtggaag 1300

tcgacctccc agtactcaag agaccagtag cagcctcttg ccacagagcc 1350

cagcccccac agaacacctg aactcaaatg agatgccgga ggacagcagc 1400

actcccgaag agatgccacc tccagagccc ccagagccac cacaggaggc 1450

agctgaagct gagaagtagc ctatctatgg aagagacttt tgtttgtgtt 1500

taattagggc tatgagagat ttcaggtgag aagttaaacc tgagacagag 1550

agcaagtaag ctgtcccttt taactgtttt tctttggtct ttagtcaccc 1600

agttgcacac tggcattttc ttgctgcaag ctttttttaaa tttctgaact 1650

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aggcctgcag aggccctgaa tgcacaaatg ggaaaccaag gcacagagag 2250

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gctaaccagt tcttccatta agcctcggct gagtgaggga aagcccagca 2350

ctgctgccct ctcgggtaac tcaccctaag gcctcggccc acctctggct 2400

atggtaacca cactgggggc ttcctccaag ccccgctctt ccagcacttc 2450

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cagtcagctc tgctcaggac ctgctctatt tcagggaaga agatttatgt 2550 attatatgtg gctatatttc ctagagcacc tgtgttttcc tctttctaag 2600

ccagggtcct gtctggatga cttatgcggt gggggagtgt aaaccggaac 2650

ttttcatcta tttgaaggcg attaaactgt gtctaatgca 2690

<210> 515
<211> 364
<212> PRT
<213> Homo sapiens

<400> 515

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				20					25					30
Met	Ala	Arg	Gln	Lys	Gly	Ile	Phe	Tyr	Leu	Thr	Leu	Phe	Leu	Ile
				35					40					45
Leu	Gly	Thr	Cys	Thr	Leu	Phe	Phe	Ala	Phe	Glu	Cys	Arg	Tyr	Leu
				50					55					60
Ala	Val	Gln	Leu	Ser	Pro	Ala	Ile	Pro	Val	Phe	Ala	Ala	Met	Leu
				65					70					75
Phe	Leu	Phe	Ser	Met	Ala	Thr	Leu	Leu	Arg	Thr	Ser	Phe	Ser	Asp
				80					85					90
Pro	Gly	Val	Ile	Pro	Arg	Ala	Leu	Pro	Asp	Glu	Ala	Ala	Phe	Ile
				95					100					105
Glu	Met	Glu	Ile	Glu	Ala	Thr	Asn	Gly	Ala	Val	Pro	Gln	Gly	Gln
				110					115					120
Arg	Pro	Pro	Pro	Arg	Ile	Lys	Asn	Phe	Gln	Ile	Asn	Asn	Gln	Ile
				125					130					135
Val	Lys	Leu	Lys	Tyr	Cys	Tyr	Thr	Cys	Lys	Ile	Phe	Arg	Pro	Pro
				140					145					150
Arg	Ala	Ser	His	Cys	Ser	Ile	Cys	Asp	Asn	Cys	Val	Glu	Arg	Phe
				155					160					165
Asp	His	His	Cys	Pro	Trp	Val	Gly	Asn	Cys	Val	Gly	Lys	Arg	Asn
				170					175					180
Tyr	Arg	Tyr	Phe	Tyr	Leu	Phe	Ile	Leu	Ser	Leu	Ser	Leu	Leu	Thr
				185					190					195
Ile	Tyr	Val	Phe	Ala	Phe	Asn	Ile	Val	Tyr	Val	Ala	Leu	Lys	Ser
				200					205					210
Leu	Lys	Ile	Gly	Phe	Leu	Glu	Thr	Leu	Lys	Glu	Thr	Pro	Gly	Thr
				215					220					225
Val	Leu	Glu	Val	Leu	Ile	Cys	Phe	Phe	Thr	Leu	Trp	Ser	Val	Val

```
                230                 235                 240

Gly Leu Thr Gly Phe His Thr Phe Leu Val Ala Leu Asn Gln Thr
                245                 250                 255

Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val
                260                 265                 270

Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asn Cys Cys Glu
                275                 280                 285

Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly
                290                 295                 300

Ile Leu Pro Leu Glu Glu Ser Gly Ser Arg Pro Pro Ser Thr Gln
                305                 310                 315

Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu
                320                 325                 330

His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu
                335                 340                 345

Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala
                350                 355                 360

Glu Ala Glu Lys
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<210> 516
<211> 255
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 36, 38, 88, 118, 135, 193, 213, 222
<223> unknown base

<400> 516

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tgaattaggt attataggga tggtggggtt gatttttntt cctggaggct 100

tttggctttg gactctcnct ttctcccaca gagcncttcg accatcactg 150

cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200

tcttcatcct ttntctctcc cncctcacaa tctatgtctt cgccttcaac 250

atcgt 255
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<210> 517
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 517
caacgtgatt tcaaagctgg gctc 24

<210> 518
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 518
gcctcgtatc aagaatttcc 20

<210> 519
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 519
agtggaagtc gacctccc 18

<210> 520
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 520
ctcacctgaa atctctcata gccc 24

<210> 521
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 521
cgcaaaaccc attttgggag caggaattcc aatcatgtct gtgatggtgg 50

<210> 522
<211> 1679
<212> DNA
<213> Homo sapiens

<400> 522
gttgtgtcct tcagcaaaac agtggattta aatctccttg cacaagcttg 50

agagcaacac aatctatcag gaaagaaaga aagaaaaaaa ccgaacctga 100

caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150
aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200
tgtgtctctt ccaaggagtg cccgtgcgca gcggagatgc caccttcccc 250
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ccatcctcta tgctgggaat gacaagtggt gcctggatcc tcgcgtggtc 400
cttctgagca acacccaaac gcagtacagc atcgagatcc agaacgtgga 450
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aaaaagaaat tgaaaattgc cttgcagata tttaggtaca atggagtttt 1400
cttttcccaa acgggaagaa cacagcacac ccggcttgga cccactgcaa 1450
gctgcatcgt gcaacctctt tggtgccagt gtgggcaagg gctcagcctc 1500
tctgcccaca gagtgccccc acgtggaaca ttctggagct ggccatccca 1550

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aattcaatca gtccatagag acgaacagaa tgagaccttc cggcccaagc 1600

gtggcgctgc gggcactttg gtagactgtg ccaccacggc gtgtgttgtg 1650

aaacgtgaaa taaaaagagc aaaaaaaaa 1679
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<210> 523
<211> 344
<212> PRT
<213> Homo sapiens

<400> 523
Met Lys Thr Ile Gln Pro Lys Met His Asn Ser Ile Ser Trp Ala
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Ile Phe Thr Gly Leu Ala Ala Leu Cys Leu Phe Gln Gly Val Pro
                20                  25                  30

Val Arg Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp Asn Val
                35                  40                  45

Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp
                50                  55                  60

Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu
                65                  70                  75

Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu
                80                  85                  90

Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val
                95                 100                 105

Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp
               110                 115                 120

Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser
               125                 130                 135

Pro Lys Ile Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly
               140                 145                 150

Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro
               155                 160                 165

Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala Val Gly Phe Val
               170                 175                 180

Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln
               185                 190                 195

Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro
               200                 205                 210

Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile
               215                 220                 225

Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr
```

230 235 240

Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp
245 250 255

Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys
260 265 270

Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val
275 280 285

Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys
290 295 300

Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala
305 310 315

Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val
320 325 330

Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe
335 340

<210> 524
<211> 503
<212> DNA
<213> Homo sapiens

<400> 524
gaaaaaaaat catgaaaacc atccagccaa aaatgcacaa ttctatctct 50

tgggcaatct tcacggggct ggctgctctg tgtctcttcc aaggagtgcc 100

cgtgcgcagc ggagatgcca ccttccccaa agctatggac aacgtgacgg 150

tccggcaggg ggagagcgcc accctcaggt gcactattga caaccgggtc 200

acccgggtgg cctggctaaa ccgcagcacc atcctctatg ctgggaatga 250

caagtggtgc ctggatcctc gcgtggtcct tctgagcaac acccaaacgc 300

agtacagcat cgagatccag aacgtggatg tgtatgacga gggcccttac 350

acctgctcgg tgcagacaga caaccaccca aagacctcta gggtccacct 400

cattgtgcaa gtatctccca aaattgtaga gatttcttca gatatctcca 450

ttaatgaagg gaacaatatt agcctcacct gcatagcaac tggtagacca 500

gag 503

<210> 525
<211> 2602
<212> DNA
<213> Homo sapiens

<400> 525
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tgaacgtcgc gctgcaggag ctgggagctg gcagcaacgt gggattccag 150

aaggggacaa gacagctgtt aggctcacgc acgcagctgg agctggtctt 200

agcaggtgcc tctctactgc tggctgcact gcttctgggc tgccttgtgg 250

ccctaggggt ccagtaccac agagacccat cccacagcac ctgccttaca 300

gaggcctgca ttcgagtggc tggaaaaatc ctggagtccc tggaccgagg 350

ggtgagcccc tgtgaggact tttaccagtt ctcctgtggg ggctggattc 400

ggaggaaccc cctgccccgat gggcgttctc gctggaacac cttcaacagc 450

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cttcaactcc agcagtgaag ctgagcagaa gacacagcgc ttctacctat 550

cttgcctaca ggtggagcgc attgaggagc tgggagccca gccactgaga 600

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cctccagcag agcccccacc attcactgtg acatctttcc gtgtcaccct 2550

gcctggaaga ggtctgggtg gggaggccag ttcccatagg aaggagtctg 2600

cc 2602

<210> 526
<211> 736
<212> PRT
<213> Homo sapiens

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<400> 526
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Phe Gln Lys Gly Thr Arg Gln Leu Leu Gly Ser Arg Thr Gln Leu
            20                  25                  30
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Glu Leu Val Leu Ala Gly Ala Ser Leu Leu Leu Ala Ala Leu Leu
35 40 45

Leu Gly Cys Leu Val Ala Leu Gly Val Gln Tyr His Arg Asp Pro
50 55 60

Ser His Ser Thr Cys Leu Thr Glu Ala Cys Ile Arg Val Ala Gly
65 70 75

Lys Ile Leu Glu Ser Leu Asp Arg Gly Val Ser Pro Cys Glu Asp
80 85 90

Phe Tyr Gln Phe Ser Cys Gly Gly Trp Ile Arg Arg Asn Pro Leu
95 100 105

Pro Asp Gly Arg Ser Arg Trp Asn Thr Phe Asn Ser Leu Trp Asp
110 115 120

Gln Asn Gln Ala Ile Leu Lys His Leu Leu Glu Asn Thr Thr Phe
125 130 135

Asn Ser Ser Ser Glu Ala Glu Gln Lys Thr Gln Arg Phe Tyr Leu
140 145 150

Ser Cys Leu Gln Val Glu Arg Ile Glu Glu Leu Gly Ala Gln Pro
155 160 165

Leu Arg Asp Leu Ile Glu Lys Ile Gly Gly Trp Asn Ile Thr Gly
170 175 180

Pro Trp Asp Gln Asp Asn Phe Met Glu Val Leu Lys Ala Val Ala
185 190 195

Gly Thr Tyr Arg Ala Thr Pro Phe Phe Thr Val Tyr Ile Ser Ala
200 205 210

Asp Ser Lys Ser Ser Asn Ser Asn Val Ile Gln Val Asp Gln Ser
215 220 225

Gly Leu Phe Leu Pro Ser Arg Asp Tyr Tyr Leu Asn Arg Thr Ala
230 235 240

Asn Glu Lys Val Leu Thr Ala Tyr Leu Asp Tyr Met Glu Glu Leu
245 250 255

Gly Met Leu Leu Gly Gly Arg Pro Thr Ser Thr Arg Glu Gln Met
260 265 270

Gln Gln Val Leu Glu Leu Glu Ile Gln Leu Ala Asn Ile Thr Val
275 280 285

Pro Gln Asp Gln Arg Arg Asp Glu Glu Lys Ile Tyr His Lys Met
290 295 300

Ser Ile Ser Glu Leu Gln Ala Leu Ala Pro Ser Met Asp Trp Leu
305 310 315

Glu Phe Leu Ser Phe Leu Leu Ser Pro Leu Glu Leu Ser Asp Ser

320 325 330

Glu Pro Val Val Val Tyr Gly Met Asp Tyr Leu Gln Gln Val Ser
335 340 345

Glu Leu Ile Asn Arg Thr Glu Pro Ser Ile Leu Asn Asn Tyr Leu
350 355 360

Ile Trp Asn Leu Val Gln Lys Thr Thr Ser Ser Leu Asp Arg Arg
365 370 375

Phe Glu Ser Ala Gln Glu Lys Leu Leu Glu Thr Leu Tyr Gly Thr
380 385 390

Lys Lys Ser Cys Val Pro Arg Trp Gln Thr Cys Ile Ser Asn Thr
395 400 405

Asp Asp Ala Leu Gly Phe Ala Leu Gly Ser Leu Phe Val Lys Ala
410 415 420

Thr Phe Asp Arg Gln Ser Lys Glu Ile Ala Glu Gly Met Ile Ser
425 430 435

Glu Ile Arg Thr Ala Phe Glu Glu Ala Leu Gly Gln Leu Val Trp
440 445 450

Met Asp Glu Lys Thr Arg Gln Ala Ala Lys Glu Lys Ala Asp Ala
455 460 465

Ile Tyr Asp Met Ile Gly Phe Pro Asp Phe Ile Leu Glu Pro Lys
470 475 480

Glu Leu Asp Asp Val Tyr Asp Gly Tyr Glu Ile Ser Glu Asp Ser
485 490 495

Phe Phe Gln Asn Met Leu Asn Leu Tyr Asn Phe Ser Ala Lys Val
500 505 510

Met Ala Asp Gln Leu Arg Lys Pro Pro Ser Arg Asp Gln Trp Ser
515 520 525

Met Thr Pro Gln Thr Val Asn Ala Tyr Tyr Leu Pro Thr Lys Asn
530 535 540

Glu Ile Val Phe Pro Ala Gly Ile Leu Gln Ala Pro Phe Tyr Ala
545 550 555

Arg Asn His Pro Lys Ala Leu Asn Phe Gly Gly Ile Gly Val Val
560 565 570

Met Gly His Glu Leu Thr His Ala Phe Asp Asp Gln Gly Arg Glu
575 580 585

Tyr Asp Lys Glu Gly Asn Leu Arg Pro Trp Trp Gln Asn Glu Ser
590 595 600

Leu Ala Ala Phe Arg Asn His Thr Ala Cys Met Glu Glu Gln Tyr
605 610 615

```
Asn Gln Tyr Gln Val Asn Gly Glu Arg Leu Asn Gly Arg Gln Thr
                620                 625                 630

Leu Gly Glu Asn Ile Thr Asp Asn Gly Gly Leu Lys Ala Ala Tyr
                635                 640                 645

Asn Ala Tyr Lys Ala Trp Leu Arg Lys His Gly Glu Glu Gln Gln
                650                 655                 660

Leu Pro Ala Val Gly Leu Thr Asn His Gln Leu Phe Phe Val Gly
                665                 670                 675

Phe Ala Gln Val Trp Cys Ser Val Arg Thr Pro Glu Ser Ser His
                680                 685                 690

Glu Gly Leu Val Thr Asp Pro His Ser Pro Ala Arg Phe Arg Val
                695                 700                 705

Leu Gly Thr Leu Ser Asn Ser Arg Asp Phe Leu Arg His Phe Gly
                710                 715                 720

Cys Pro Val Gly Ser Pro Met Asn Pro Gly Gln Leu Cys Glu Val
                725                 730                 735

Trp


<210> 527
<211> 4308
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1478, 3978, 4057-4058, 4070
<223> unknown base

<400> 527
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cgcgccctcc tccctccctc ctccccagct gtcccgttcg cgtcatgccg 100

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caagcccgtc cccgcaggct gcaccttcgg cgggaaggtc tatgccttgg 500
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agggtgcctg gctgaaccgg tcaagtatta tttttgcggg aggtgataag 550

tggtcagtgg atcctcgagt ttcaatttca acattgaata aaagggacta 600

cagcctccag atacagaatg tagatgtgac agatgatggc ccatacacgt 650

gttctgttca gactcaacat acacccagaa caatgcaggt gcatctaact 700

gtgcaagttc ctcctaagat atatgacatc tcaaatgata tgaccgtcaa 750

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aagttgttgt caactttgct cctactattc aggaaattaa atctggcacc 1000

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gcctccagcc tttgaatggt acaaaggaga gaagaagctc ttcaatggcc 1100

aacaaggaat tattattcaa aattttagca caagatccat tctcactgtt 1150

accaacgtga cacaggagca cttcggcaat tatacctgtg tggctgccaa 1200

caagctaggc acaaccaatg cgagcctgcc tcttaaccct ccaagtacag 1250 cccagtatgg aattaccggg agcgctgatg ttcttttctc ctgctggtac 1300

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aaagtgctga tggctggatc caatctggta cagtttgtta aaagcagcgt 1450

gggatataat cagcagtgct tacatgggga tgatcgcctt ctgtagaatt 1500

gctcattatg taaatacttt aattctactc ttttttgatt agctacatta 1550

ccttgtgaag cagtacacat tgtccttttt ttaagacgtg aaagctctga 1600

aattactttt agaggatatt aattgtgatt tcatgtttgt aatctacaac 1650

ttttcaaaag cattcagtca tggtctgcta ggttgcaggc tgtagtttac 1700

aaaaacgaat attgcagtga atatgtgatt ctttaaggct gcaatacaag 1750

cattcagttc cctgtttcaa taagagtcaa tccacattta caaagatgca 1800

ttttttttctt ttttgataaa aaagcaaata atattgcctt cagattattt 1850

cttcaaaata taacacatat ctagattttt ctgcttgcat gatattcagg 1900

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caaaaatttt aagatgattt gtcagaaagg gcacaaagtc ctatcaccta 2400

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tattatgaca gtcgacctgg agggtatgga tatggatatg gacgttccag 2500

agactataat ggcagaaacc agggtggtta tgaccgctac tcaggaggaa 2550

attacagaga caattatgac aactgaaatg agacatgcac ataatataga 2600

tacacaagga ataatttctg atccaggatc gtccttccaa atggctgtat 2650

ttataaaggt ttttggagct gcactgaagc atcttatttt atagtatatc 2700 aacctttttgt ttttaaattg acctgccaag gtagctgaag accttttaga 2750

cagttccatc ttttttttta aattttttct gcctatttaa agacaaatta 2800

tgggacgttt gtcaaaaaa aaaaaaaaaa aaaaaaaaaa 2840

<210> 612
<211> 352
<212> PRT
<213> Homo Sapien

<400> 612
Met Met Leu Leu Val Gln Gly Ala Cys Cys Ser Asn Gln Trp Leu
1 5 10 15

Ala Ala Val Leu Leu Ser Leu Cys Cys Leu Leu Pro Ser Cys Leu
20 25 30

Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val Asp Asn
35 40 45

Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu
50 55 60

Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile
65 70 75

Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser
80 85 90

Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn
95 100 105

Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr
110 115 120

Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val Gln Val
125 130 135

Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu
140 145 150

Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu
155 160 165

Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe
170 175 180

Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln
185 190 195

Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Ala Val Ser Phe Pro
200 205 210

Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro Thr Ile
215 220 225

Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser Gly Leu

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                 230                 235                 240

Ile Arg Cys Glu Gly Ala Gly Val Pro Pro Pro Ala Phe Glu Trp
                245                 250                 255

Tyr Lys Gly Glu Lys Lys Leu Phe Asn Gly Gln Gln Gly Ile Ile
                260                 265                 270

Ile Gln Asn Phe Ser Thr Arg Ser Ile Leu Thr Val Thr Asn Val
                275                 280                 285

Thr Gln Glu His Phe Gly Asn Tyr Thr Cys Val Ala Ala Asn Lys
                290                 295                 300

Leu Gly Thr Thr Asn Ala Ser Leu Pro Leu Asn Pro Pro Ser Thr
                305                 310                 315

Ala Gln Tyr Gly Ile Thr Gly Ser Ala Asp Val Leu Phe Ser Cys
                320                 325                 330

Trp Tyr Leu Val Leu Thr Leu Ser Ser Phe Thr Ser Ile Phe Tyr
                335                 340                 345

Leu Lys Asn Ala Ile Leu Gln
                350
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<210> 613
<211> 1797
<212> DNA
<213> Homo Sapien

<400> 613
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aaataagaaa attctcaagg aggacgagct cttgagtgag acccaacaag 150

ctgcttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200

cccaagagga gaaatggggt gaacttctcc ctagctgtgg tggtcatcta 250

cctgatcctg ctcaccgctg gcgctgggct gctggtggtc caagttctga 300

atctgcaggc gcggctccgg gtcctggaga tgtatttcct caatgacact 350

ctggcggctg aggacagccc gtccttctcc ttgctgcagt cagcacaccc 400

tggagaacac ctggctcagg gtgcatcgag gctgcaagtc ctgcaggccc 450

aactcacctg ggtccgcgtc agccatgagc acttgctgca gcgggtagac 500

aacttcactc agaacccagg gatgttcaga atcaaaggtg aacaaggcgc 550

cccaggtctt caaggtcaca aggggggccat gggcatgcct ggtgcccctg 600

gcccgccggg accacctgct gagaagggag ccaagggggc tatgggacga 650

gatggagcaa caggcccctc gggaccccaa ggcccaccgg gagtcaaggg 700
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ctggcacccc aggaccccaa ggagagaagg gcagcaaagg cgatgggggt 800
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tcatggggcc tcctggagcc caggggagta aaggtgactt cgggaggcca 950
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ccagggagcc ccgggagtcc aggagccaca ggcctgaaag gaagcaaagg 1150
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<210> 614
<211> 520
<212> PRT
<213> Homo Sapien

<400> 614
Met Arg Asn Lys Lys Ile Leu Lys Glu Asp Glu Leu Leu Ser Glu
1 5 10 15

Thr Gln Gln Ala Ala Phe His Gln Ile Ala Met Glu Pro Phe Glu
20 25 30

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Ile Asn Val Pro Lys Pro Lys Arg Arg Asn Gly Val Asn Phe Ser
                35                  40                  45

Leu Ala Val Val Val Ile Tyr Leu Ile Leu Leu Thr Ala Gly Ala
                50                  55                  60

Gly Leu Leu Val Val Gln Val Leu Asn Leu Gln Ala Arg Leu Arg
                65                  70                  75

Val Leu Glu Met Tyr Phe Leu Asn Asp Thr Leu Ala Ala Glu Asp
                80                  85                  90

Ser Pro Ser Phe Ser Leu Leu Gln Ser Ala His Pro Gly Glu His
                95                  100                 105

Leu Ala Gln Gly Ala Ser Arg Leu Gln Val Leu Gln Ala Gln Leu
                110                 115                 120

Thr Trp Val Arg Val Ser His Glu His Leu Leu Gln Arg Val Asp
                125                 130                 135

Asn Phe Thr Gln Asn Pro Gly Met Phe Arg Ile Lys Gly Glu Gln
                140                 145                 150

Gly Ala Pro Gly Leu Gln Gly His Lys Gly Ala Met Gly Met Pro
                155                 160                 165

Gly Ala Pro Gly Pro Pro Gly Pro Pro Ala Glu Lys Gly Ala Lys
                170                 175                 180

Gly Ala Met Gly Arg Asp Gly Ala Thr Gly Pro Ser Gly Pro Gln
                185                 190                 195

Gly Pro Pro Gly Val Lys Gly Glu Ala Gly Leu Gln Gly Pro Gln
                200                 205                 210

Gly Ala Pro Gly Lys Gln Gly Ala Thr Gly Thr Pro Gly Pro Gln
                215                 220                 225

Gly Glu Lys Gly Ser Lys Gly Asp Gly Gly Leu Ile Gly Pro Lys
                230                 235                 240

Gly Glu Thr Gly Thr Lys Gly Glu Lys Gly Asp Leu Gly Leu Pro
                245                 250                 255

Gly Ser Lys Gly Asp Arg Gly Met Lys Gly Asp Ala Gly Val Met
                260                 265                 270

Gly Pro Pro Gly Ala Gln Gly Ser Lys Gly Asp Phe Gly Arg Pro
                275                 280                 285

Gly Pro Pro Gly Leu Ala Gly Phe Pro Gly Ala Lys Gly Asp Gln
                290                 295                 300

Gly Gln Pro Gly Leu Gln Gly Val Pro Gly Pro Pro Gly Ala Val
                305                 310                 315

Gly His Pro Gly Ala Lys Gly Glu Pro Gly Ser Ala Gly Ser Pro
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320 325 330

Gly Arg Ala Gly Leu Pro Gly Ser Pro Gly Ser Pro Gly Ala Thr
335 340 345

Gly Leu Lys Gly Ser Lys Gly Asp Thr Gly Leu Gln Gly Gln Gln
350 355 360

Gly Arg Lys Gly Glu Ser Gly Val Pro Gly Pro Ala Gly Val Lys
365 370 375

Gly Glu Gln Gly Ser Pro Gly Leu Ala Gly Pro Lys Gly Ala Pro
380 385 390

Gly Gln Ala Gly Gln Lys Gly Asp Gln Gly Val Lys Gly Ser Ser
395 400 405

Gly Glu Gln Gly Val Lys Gly Glu Lys Gly Glu Arg Gly Glu Asn
410 415 420

Ser Val Ser Val Arg Ile Val Gly Ser Ser Asn Arg Gly Arg Ala
425 430 435

Glu Val Tyr Tyr Ser Gly Thr Trp Gly Thr Ile Cys Asp Asp Glu
440 445 450

Trp Gln Asn Ser Asp Ala Ile Val Phe Cys Arg Met Leu Gly Tyr
455 460 465

Ser Lys Gly Arg Ala Leu Tyr Lys Val Gly Ala Gly Thr Gly Gln
470 475 480

Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu
485 490 495

Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His
500 505 510

Glu Glu Asp Ala Gly Val Glu Cys Ser Val
515 520

<210> 615
<211> 647
<212> DNA
<213> Homo Sapien

<400> 615
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agcacctcct ctcttctcct tttgcccaaa ctcacccagt gagtgtgagc 100

atttaagaag catcctctgc caagaccaaa aggaaagaag aaaaagggcc 150

aaaagccaaa atgaaactga tggtacttgt tttcaccatt gggctaactt 200

tgctgctagg agttcaagcc atgcctgcaa atcgcctctc ttgctacaga 250

aagatactaa aagatcacaa ctgtcacaac cttccggaag gagtagctga 300 cctgacacag attgatgtca atgtccagga tcatttctgg gatgggaagg 350

gatgtgagat gatctgttac tgcaacttca gcgaattgct ctgctgccca 400

aaagacgttt tctttggacc aaagatctct ttcgtgattc cttgcaacaa 450

tcaatgagaa tcttcatgta ttctggagaa caccattcct gatttcccac 500

aaactgcact acatcagtat aactgcattt ctagtttcta tatagtgcaa 550

tagagcatag attctataaa ttcttacttg tctaagacaa gtaaatctgt 600

gttaaacaag tagtaataaa agttaattca atctaaaaaa aaaaaaa 647

<210> 616
<211> 98
<212> PRT
<213> Homo Sapien

<400> 616
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Met Lys Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu
  1               5                  10                  15

Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg
                 20                  25                  30

Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val
                 35                  40                  45

Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp
                 50                  55                  60

Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu
                 65                  70                  75

Leu Leu Cys Cys Pro Lys Asp Val Phe Phe Gly Pro Lys Ile Ser
                 80                  85                  90

Phe Val Ile Pro Cys Asn Asn Gln
                 95
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<210> 617
<211> 2558
<212> DNA
<213> Homo Sapien

<400> 617
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cagcctgcag ggctgataag cgaggcatta gtgagattga gagagacttt 100

accccgccgt ggtggttgga gggcgcgcag tagagcagca gcacaggcgc 150

gggtcccggg aggccggctc tgctcgcgcc gagatgtgga atctccttca 200

cgaaaccgac tcggctgtgg ccaccgcgcg ccgcccgcgc tggctgtgcg 250

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taatatgaaa gcatttttgg atgaattgaa agctgagaac atcaagaagt 400

tcttacataa ttttacacag ataccacatt tagcaggaac agaacaaaac 450

tttcagcttg caaagcaaat tcaatcccag tggaaagaat ttggcctgga 500

ttctgttgag ctagctcatt atgatgtcct gttgtcctac ccaaataaga 550

ctcatcccaa ctacatctca ataattaatg aagatggaaa tgagattttc 600

aacacatcat tatttgaacc acctcctcca ggatatgaaa atgtttcgga 650

tattgtacca cctttcagtg ctttctctcc tcaaggaatg ccagagggcg 700

atctagtgta tgttaactat gcacgaactg aagacttctt taaattggaa 750

cgggacatga aaatcaattg ctctgggaaa attgtaattg ccagatatgg 800

gaaagttttc agaggaaata aggttaaaaa tgcccagctg gcaggggcca 850

aaggagtcat tctctactcc gaccctgctg actactttgc tcctggggtg 900

aagtcctatc cagacggttg gaatcttcct ggaggtggtg tccagcgtgg 950

aaatatccta aatctgaatg gtgcaggaga ccctctcaca ccaggttacc 1000

cagcaaatga atatgcttat aggcgtggaa ttgcagaggc tgttggtctt 1050

ccaagtattc ctgttcatcc aattggatac tatgatgcac agaagctcct 1100

agaaaaaatg ggtggctcag caccaccaga tagcagctgg agaggaagtc 1150

tcaaagtgcc ctacaatgtt ggacctggct ttactggaaa cttttctaca 1200

caaaaagtca agatgcacat ccactctacc aatgaagtga cgagaattta 1250

caatgtgata ggtactctca gaggagcagt ggaaccagac agatatgtca 1300

ttctgggagg tcaccgggac tcatgggtgt ttggtggtat tgaccctcag 1350

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aaaggaaggg tggagaccta gaagaacaat tttgtttgca agctgggatg 1450

cagaagaatt tggtcttctt ggttctactg agtgggcaga ggagaattca 1500

agactccttc aagagcgtgg cgtggcttat attaatgctg actcatctat 1550

agaaggaaac tacactctga gagttgattg tacaccgctg atgtacagct 1600

tggtacacaa cctaacaaaa gagctgaaaa gccctgatga aggctttgaa 1650

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cagtggcatg cccaggataa gcaaattggg atctggaaat gattttgagg 1750 tgttcttcca acgacttgga attgcttcag gcagagcacg gtatactaaa 1800

aattgggaaa caaacaaatt cagcggctat ccactgtatc acagtgtcta 1850

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acctcactgt ggcccaggtt cgaggaggga tggtgtttga gctagccaat 1950

tccatagtgc tcccttttga ttgtcgagat tatgctgtag ttttaagaaa 2000

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acagaaattg cttccaagtt cagtgagaga ctccaggact ttgacaaaag 2150

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gagcatttat tgatccatta gggttaccag acaggccttt ttataggcat 2250

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aggcctgggg agaagtgaag agacagattt atgttgcagc cttcacagtg 2400

caggcagctg cagagacttt gagtgaagta gcctaagagg atttttaga 2450

gaatccgtat tgaatttgtg tggtatgtca ctcagaaaga atcgtaatgg 2500

gtatattgat aaattttaaa attggtatat ttgaaataaa gttgaatatt 2550

atatataa 2558

<210> 618
<211> 750
<212> PRT
<213> Homo Sapien

<400> 618

Met	Trp	Asn	Leu	Leu	His	Glu	Thr	Asp	Ser	Ala	Val	Ala	Thr	Ala
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Arg	Arg	Pro	Arg	Trp	Leu	Cys	Ala	Gly	Ala	Leu	Val	Leu	Ala	Gly
				20					25					30
Gly	Phe	Phe	Leu	Leu	Gly	Phe	Leu	Phe	Gly	Trp	Phe	Ile	Lys	Ser
				35					40					45
Ser	Asn	Glu	Ala	Thr	Asn	Ile	Thr	Pro	Lys	His	Asn	Met	Lys	Ala
				50					55					60
Phe	Leu	Asp	Glu	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Lys	Phe	Leu	His
				65					70					75
Asn	Phe	Thr	Gln	Ile	Pro	His	Leu	Ala	Gly	Thr	Glu	Gln	Asn	Phe
				80					85					90

Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu
95 100 105

Asp Ser Val Glu Leu Ala His Tyr Asp Val Leu Leu Ser Tyr Pro
110 115 120

Asn Lys Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly
125 130 135

Asn Glu Ile Phe Asn Thr Ser Leu Phe Glu Pro Pro Pro Pro Gly
140 145 150

Tyr Glu Asn Val Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser
155 160 165

Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala
170 175 180

Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile Asn
185 190 195

Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg
200 205 210

Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly Val
215 220 225

Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
230 235 240

Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg
245 250 255

Gly Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro
260 265 270

Gly Tyr Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu
275 280 285

Ala Val Gly Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr
290 295 300

Asp Ala Gln Lys Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro
305 310 315

Asp Ser Ser Trp Arg Gly Ser Leu Lys Val Pro Tyr Asn Val Gly
320 325 330

Pro Gly Phe Thr Gly Asn Phe Ser Thr Gln Lys Val Lys Met His
335 340 345

Ile His Ser Thr Asn Glu Val Thr Arg Ile Tyr Asn Val Ile Gly
350 355 360

Thr Leu Arg Gly Ala Val Glu Pro Asp Arg Tyr Val Ile Leu Gly
365 370 375

Gly His Arg Asp Ser Trp Val Phe Gly Gly Ile Asp Pro Gln Ser

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                380                 385                 390

Gly Ala Ala Val Val His Glu Ile Val Arg Ser Phe Gly Thr Leu
                395                 400                 405

Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile Leu Phe Ala Ser
                410                 415                 420

Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr Glu Trp Ala
                425                 430                 435

Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala Tyr Ile
                440                 445                 450

Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val Asp
                455                 460                 465

Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu
                470                 475                 480

Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu
                485                 490                 495

Ser Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro
                500                 505                 510

Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe
                515                 520                 525

Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn
                530                 535                 540

Trp Glu Thr Asn Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val
                545                 550                 555

Tyr Glu Thr Tyr Glu Leu Val Glu Lys Phe Tyr Asp Pro Met Phe
                560                 565                 570

Lys Tyr His Leu Thr Val Ala Gln Val Arg Gly Gly Met Val Phe
                575                 580                 585

Glu Leu Ala Asn Ser Ile Val Leu Pro Phe Asp Cys Arg Asp Tyr
                590                 595                 600

Ala Val Val Leu Arg Lys Tyr Ala Asp Lys Ile Tyr Ser Ile Ser
                605                 610                 615

Met Lys His Pro Gln Glu Met Lys Thr Tyr Ser Val Ser Phe Asp
                620                 625                 630

Ser Leu Phe Ser Ala Val Lys Asn Phe Thr Glu Ile Ala Ser Lys
                635                 640                 645

Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser Asn Pro Ile Val
                650                 655                 660

Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu Arg Ala Phe
                665                 670                 675
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Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg His Val
                680                 685                 690

Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser Phe
                695                 700                 705

Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
                710                 715                 720

Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala
                725                 730                 735

Ala Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
                740                 745                 750
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<210> 619
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 619
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<210> 620
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 620
gaacatcagc gctcccggta attcc 25

<210> 621
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 621
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<211> 25
<212> DNA
<213> Artificial Sequence

<220>
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<210> 623
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